

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:18 ; Search time 32.5171 Seconds
(without alignments)
165.965 Million cell updates/sec

Title: US-09-843-221A-164
Perfect score: 34
Sequence: 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75810

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	34	100.0	34	23	AAU73031	Parathyroid hormon	
2	34	100.0	35	23	AAU73175	Parathyroid hormon	
3	34	100.0	38	15	AAR58136	[Arg19]-hPTH(1-38)	
4	30	88.2	30	23	AAU73054	Parathyroid hormon	
5	28	82.4	28	21	AAU98046	Human parathyroid	
6	27	79.4	28	21	AAU98042	Human parathyroid	
7	27	79.4	28	21	AAU98044	Human parathyroid	
8	24	70.6	34	18	AAW08130	Human PTH derivati	
9	20	58.8	34	13	AAR22297	Human parathyroid	
10	20	58.8	34	22	AAB84828	Parathyroid hormon	
11	20	58.8	34	22	AAB96921	Parathyroid hormon	
12	18	52.9	28	17	AAR88837	Human parathyroid	
13	18	52.9	28	17	AAR88838	Human parathyroid	
14	18	52.9	28	21	AAU98052	Human parathyroid	
15	18	52.9	28	22	AAB81074	Human parathyroid	
16	18	52.9	28	23	AAU73064	Parathyroid hormon	
17	18	52.9	29	12	AAR11731	Adenine-rich PTH-(
18	18	52.9	29	17	AAR88836	Human parathyroid	
19	18	52.9	29	17	AAR88839	Human parathyroid	
20	18	52.9	29	22	AAB81075	Human parathyroid	
21	18	52.9	29	23	AAU73063	Parathyroid hormon	
22	18	52.9	29	23	AAU73179	Parathyroid hormon	
23	18	52.9	30	17	AAR88832	Human parathyroid	
24	18	52.9	30	17	AAR88833	Human parathyroid	
25	18	52.9	30	19	AAW42052	Human parathyroid	
26	18	52.9	30	23	AAU73051	Parathyroid hormon	
27	18	52.9	30	23	AAU73062	Parathyroid hormon	
28	18	52.9	30	23	AAU73136	Parathyroid hormon	
29	18	52.9	30	23	AAU73137	Parathyroid hormon	
30	18	52.9	30	23	AAU73138	Parathyroid hormon	
31	18	52.9	30	23	AAU73139	Parathyroid hormon	
32	18	52.9	30	23	AAU73178	Parathyroid hormon	
33	18	52.9	31	19	AAW42056	Human parathyroid	
34	18	52.9	31	19	AAW42057	Human parathyroid	
35	18	52.9	31	19	AAW42059	Human parathyroid	
36	18	52.9	31	19	AAW42060	Human parathyroid	
37	18	52.9	31	19	AAW42062	Human parathyroid	
38	18	52.9	31	19	AAW42063	Human parathyroid	
39	18	52.9	31	19	AAW42065	Human parathyroid	
40	18	52.9	31	19	AAW42066	Human parathyroid	
41	18	52.9	31	19	AAW42067	Human parathyroid	
42	18	52.9	31	19	AAW42049	Human parathyroid	
43	18	52.9	31	19	AAW42050	Human parathyroid	
44	18	52.9	31	19	AAW42051	Human parathyroid	
45	18	52.9	31	19	AAW42053	Human parathyroid	
46	18	52.9	31	20	AAU02578	N-terminal 31 resi	
47	18	52.9	31	22	AAB81080	Human parathyroid	
48	18	52.9	31	22	AAB91097	Parathyroid hormon	
49	18	52.9	31	23	AAE23720	Human parathyroid	
50	18	52.9	31	23	AAU73039	Parathyroid hormon	

51	18	52.9	31	23	AAU73040	Parathyroid hormon
52	18	52.9	31	23	AAU73177	Parathyroid hormon
53	18	52.9	31	23	AAU82640	Analogue of human
54	18	52.9	32	23	AAU73176	Parathyroid hormon
55	18	52.9	33	9	AAP82176	Sequence of parath
56	18	52.9	33	21	AAV98018	Human amino-termin
57	18	52.9	34	4	AAP30022	Human parathyroid-
58	18	52.9	34	6	AAP50377	[Met(O)8,18]hPTH-(
59	18	52.9	34	7	AAP60031	Sequence of the fi
60	18	52.9	34	11	AAR07919	Human parathyroid
61	18	52.9	34	11	AAR07922	Human parathyroid
62	18	52.9	34	13	AAR22283	Parathyroid hormon
63	18	52.9	34	13	AAR22298	Human parathyroid
64	18	52.9	34	13	AAR22299	Human parathyroid
65	18	52.9	34	14	AAR34358	Human parathyroid
66	18	52.9	34	14	AAR34353	Human parathyroid
67	18	52.9	34	14	AAR34354	Human parathyroid
68	18	52.9	34	14	AAR34355	Human parathyroid
69	18	52.9	34	14	AAR34356	Human parathyroid
70	18	52.9	34	14	AAR34357	Human parathyroid
71	18	52.9	34	14	AAR34359	Human parathyroid
72	18	52.9	34	14	AAR34360	Human parathyroid
73	18	52.9	34	14	AAR34361	Human parathyroid
74	18	52.9	34	14	AAR34362	Human parathyroid
75	18	52.9	34	14	AAR34363	Human parathyroid
76	18	52.9	34	14	AAR34364	Human parathyroid
77	18	52.9	34	14	AAR34365	Human parathyroid
78	18	52.9	34	14	AAR34366	Human parathyroid
79	18	52.9	34	14	AAR34367	Human parathyroid
80	18	52.9	34	14	AAR34368	Human parathyroid
81	18	52.9	34	14	AAR34456	Human parathyroid
82	18	52.9	34	14	AAR34457	Human parathyroid
83	18	52.9	34	14	AAR41549	[D-Ser3]hPTH (1-34
84	18	52.9	34	14	AAR41554	[Thr27]hPTH (1-34)
85	18	52.9	34	14	AAR41555	[Asn27]hPTH (1-34)
86	18	52.9	34	14	AAR41556	[Gln26,27]hPTH (1-
87	18	52.9	34	14	AAR41557	[Gln25,26,27]hPTH
88	18	52.9	34	14	AAR41558	[Ser27]hPTH (1-34)
89	18	52.9	34	14	AAR41559	[Gly27]hPTH (1-34)
90	18	52.9	34	14	AAR41560	[His27]hPTH (1-34)
91	18	52.9	34	14	AAR41566	[Arg 26,27]hPTH (1
92	18	52.9	34	14	AAR41567	[Gln26]hPTH (1-34)
93	18	52.9	34	14	AAR41570	[Gln25]hPTH (1-34)
94	18	52.9	34	15	AAR58291	[Lys(For)26, Lys(F
95	18	52.9	34	15	AAR58228	[D-Asp30]-hPTH(1-3
96	18	52.9	34	15	AAR58232	[Lys32]-hPTH(1-34)
97	18	52.9	34	15	AAR58181	[Thr33, Ala34]-hPT
98	18	52.9	34	15	AAR58187	[Phe23,His25,His26
99	18	52.9	34	15	AAR58189	[F23,H25,H26,L27,I
100	18	52.9	34	15	AAR58016	N-alpha-Isopropyl-
101	18	52.9	34	15	AAR58017	[Lys(N-epsilon-Iso
102	18	52.9	34	15	AAR55724	Parathormone N-ter
103	18	52.9	34	16	AAR74521	Human parathyroid
104	18	52.9	34	17	AAW99449	Human parathyroid
105	18	52.9	34	17	AAR99978	Human parathyroid
106	18	52.9	34	17	AAR98951	Target peptide (PT
107	18	52.9	34	17	AAR98966	PTH(1-34). Not sp

108	18	52.9	34	17	AAR88829	Human parathyroid
109	18	52.9	34	17	AAR88834	Human parathyroid
110	18	52.9	34	17	AAR88835	Human parathyroid
111	18	52.9	34	18	AAW24276	Parathyroid hormon
112	18	52.9	34	18	AAW24273	Wild type parathyr
113	18	52.9	34	18	AAW19994	Cyclised human par
114	18	52.9	34	18	AAW20000	Cyclised human par
115	18	52.9	34	18	AAW20006	Cyclised human par
116	18	52.9	34	18	AAW17949	Human parathyroid
117	18	52.9	34	18	AAW17944	Human parathyroid
118	18	52.9	34	18	AAW17945	Human parathyroid
119	18	52.9	34	18	AAW17947	Human parathyroid
120	18	52.9	34	18	AAW17948	Human parathyroid
121	18	52.9	34	18	AAW17969	Human parathyroid
122	18	52.9	34	18	AAW17968	Human parathyroid
123	18	52.9	34	18	AAW17950	Human PTH analogue
124	18	52.9	34	18	AAW17951	Human parathyroid
125	18	52.9	34	18	AAW17954	Human parathyroid
126	18	52.9	34	18	AAW17955	Human parathyroid
127	18	52.9	34	18	AAW01610	Parathryoid hormon
128	18	52.9	34	19	AAW67279	Parathyroid hormon
129	18	52.9	34	19	AAW67280	Parathyroid hormon
130	18	52.9	34	19	AAW67282	Parathyroid hormon
131	18	52.9	34	19	AAW67283	Parathyroid hormon
132	18	52.9	34	19	AAW67284	Parathyroid hormon
133	18	52.9	34	19	AAW67285	Parathyroid hormon
134	18	52.9	34	19	AAW67286	Parathyroid hormon
135	18	52.9	34	19	AAW67288	Parathyroid hormon
136	18	52.9	34	19	AAW67305	Parathyroid hormon
137	18	52.9	34	19	AAW67289	Parathyroid hormon
138	18	52.9	34	19	AAW67291	Parathyroid hormon
139	18	52.9	34	19	AAW67292	Parathyroid hormon
140	18	52.9	34	19	AAW67293	Parathyroid hormon
141	18	52.9	34	19	AAW67294	Parathyroid hormon
142	18	52.9	34	19	AAW67295	Parathyroid hormon
143	18	52.9	34	19	AAW67296	Parathyroid hormon
144	18	52.9	34	19	AAW67297	Parathyroid hormon
145	18	52.9	34	19	AAW67302	Parathyroid hormon
146	18	52.9	34	19	AAW67303	Parathyroid hormon
147	18	52.9	34	19	AAW67304	Parathyroid hormon
148	18	52.9	34	19	AAW61658	Parathyroid hormon
149	18	52.9	34	19	AAW65975	Human parathyroid
150	18	52.9	34	19	AAW42614	Human parathyroid
151	18	52.9	34	19	AAW42054	Human parathyroid
152	18	52.9	34	19	AAW42055	Human parathyroid
153	18	52.9	34	19	AAW48392	Human parathyroid
154	18	52.9	34	20	AAV50593	Resin bound cyclic
155	18	52.9	34	20	AAV17752	Human parathyroid
156	18	52.9	34	20	AAV14151	Human parathyroid
157	18	52.9	34	20	AAV02579	N-terminal 34 resi
158	18	52.9	34	20	AAW81871	Human PTH N-termin
159	18	52.9	34	21	ABJ10712	Human parathyroid
160	18	52.9	34	21	AAB07454	Amino acids 1-34 o
161	18	52.9	34	21	AAV98017	Human amino-termin
162	18	52.9	34	21	AAV82631	Human parathyroid
163	18	52.9	34	21	AAV68763	Amino acids 1-34 o
164	18	52.9	34	22	AAB84778	Native rat parathy

165	18	52.9	34	22	AAB96898	Human parathyroid
166	18	52.9	34	22	AAB96929	Human parathyroid
167	18	52.9	34	22	AAB81079	Human parathyroid
168	18	52.9	34	22	AAB91098	Parathyroid hormon
169	18	52.9	34	23	ABJ05328	Human PTH(1-34) pe
170	18	52.9	34	23	AAE23727	Human parathyroid
171	18	52.9	34	23	ABB06329	Human parathyroid
172	18	52.9	34	23	ABB08595	C-terminal truncat
173	18	52.9	34	23	AAE18395	Human PTH peptide
174	18	52.9	34	23	ABB07147	Parathyroid hormon
175	18	52.9	34	23	AAU73028	Parathyroid hormon
176	18	52.9	34	23	AAU73100	Parathyroid hormon
177	18	52.9	34	23	AAU73101	Parathyroid hormon
178	18	52.9	34	23	AAU73102	Parathyroid hormon
179	18	52.9	34	23	AAU73103	Parathyroid hormon
180	18	52.9	34	23	AAU73104	Parathyroid hormon
181	18	52.9	34	23	AAU73140	Parathyroid hormon
182	18	52.9	34	24	ABP71500	Human parathyroid
183	18	52.9	34	24	ABG74235	Human parathyroid
184	18	52.9	35	22	AAB91112	Parathyroid hormon
185	18	52.9	35	23	AAU73172	Parathyroid hormon
186	18	52.9	36	14	AAR39450	Ser-Val-(hPTH 3-35
187	18	52.9	36	15	AAR58286	[D-Leu24]-hPTH(1-3
188	18	52.9	36	15	AAR58287	[Phe25]-hPTH(1-36)
189	18	52.9	36	15	AAR58288	[Lys25]-hPTH(1-36)
190	18	52.9	36	15	AAR58289	[Ala25]-hPTH(1-36)
191	18	52.9	36	15	AAR58290	[Ala26]-hPTH(1-36)
192	18	52.9	36	15	AAR58292	[D-Lys27]-hPTH(1-3
193	18	52.9	36	15	AAR58293	[D-Leu28]-hPTH(1-3
194	18	52.9	36	15	AAR58294	[D-Phe34]-hPTH(1-3
195	18	52.9	36	15	AAR58295	[D-Val35]-hPTH(1-3
196	18	52.9	36	15	AAR58296	[Ala35]-hPTH(1-36)
197	18	52.9	36	15	AAR58297	[Pro35]-hPTH(1-36)
198	18	52.9	36	15	AAR58298	[NMeVal35]-hPTH(1-
199	18	52.9	36	15	AAR58299	[Thr35,Ala36]-hPTH
200	18	52.9	36	15	AAR58300	[D-Ala36]-hPTH(1-3
201	18	52.9	36	15	AAR58301	[NMeAla36]-hPTH(1-
202	18	52.9	36	15	AAR58260	[D-Val2]-hPTH(1-36
203	18	52.9	36	15	AAR58263	[D-Ile5]-hPTH(1-36
204	18	52.9	36	15	AAR58264	[D-Gln6]-hPTH(1-36
205	18	52.9	36	15	AAR58265	[D-Leu7]-hPTH(1-36
206	18	52.9	36	15	AAR58270	[D-Leu11]-hPTH(1-3
207	18	52.9	36	15	AAR58272	[D-Lys13]-hPTH(1-3
208	18	52.9	36	15	AAR58273	[D-Leu15]-hPTH(1-3
209	18	52.9	36	15	AAR58276	[Met(O2)18]-hPTH(1
210	18	52.9	36	15	AAR58278	[D-Met18]-hPTH(1-3
211	18	52.9	36	15	AAR58279	[Lys20]-hPTH(1-36)
212	18	52.9	36	15	AAR58280	[D-Arg20]-hPTH(1-3
213	18	52.9	36	15	AAR58281	[D-Val21]-hPTH(1-3
214	18	52.9	36	15	AAR58284	[D-Trp23]-hPTH(1-3
215	18	52.9	36	15	AAR58285	[Ala23]-hPTH(1-36)
216	18	52.9	36	15	AAR58222	[His27]-hPTH(1-36)
217	18	52.9	36	15	AAR58223	[Phe27]-hPTH(1-36)
218	18	52.9	36	15	AAR58224	[Nle27]-hPTH(1-36)
219	18	52.9	36	15	AAR58225	[Asn27]-hPTH(1-36)
220	18	52.9	36	15	AAR58226	[Ala27]-hPTH(1-36)
221	18	52.9	36	15	AAR58227	[D-Gln29]-hPTH(1-3

222	18	52.9	36	15	AAR58229	[Ala30]-hPTH(1-36)
223	18	52.9	36	15	AAR58230	[D-Val31]-hPTH(1-3
224	18	52.9	36	15	AAR58231	[Ala31]-hPTH(1-36)
225	18	52.9	36	15	AAR58233	[D-His32]-hPTH(1-3
226	18	52.9	36	15	AAR58234	[Ala32]-hPTH(1-36)
227	18	52.9	36	15	AAR58235	[D-Asn33]-hPTH(1-3
228	18	52.9	36	15	AAR58236	[Ala33]-hPTH(1-36)
229	18	52.9	36	15	AAR58237	[NMePhe34]-hPTH(1-
230	18	52.9	36	15	AAR58238	[D-Asp30]-hPTH(1-3
231	18	52.9	36	15	AAR58242	[Lys(Isopropyl)13]
232	18	52.9	36	15	AAR58246	Acetyl-hPTH(1-36)-
233	18	52.9	36	15	AAR58249	[D-Ser1]-hPTH(1-36
234	18	52.9	36	15	AAR58190	[Ala29]-hPTH(1-36)
235	18	52.9	36	15	AAR58191	[Ala34]-hPTH(1-36)
236	18	52.9	36	15	AAR58192	[Gln25]-hPTH(1-36)
237	18	52.9	36	15	AAR58196	[D-Phe34, D-Ala36]
238	18	52.9	36	15	AAR58198	[D-Ser3]-hPTH(1-36
239	18	52.9	36	15	AAR58199	[D-Glu4]-hPTH(1-36
240	18	52.9	36	15	AAR58200	[D-His9]-hPTH(1-36
241	18	52.9	36	15	AAR58202	[D-Asn10]-hPTH(1-3
242	18	52.9	36	15	AAR58210	[D-His14]-hPTH(1-3
243	18	52.9	36	15	AAR58211	[D-Asn16]-hPTH(1-3
244	18	52.9	36	15	AAR58213	[D-Ser17]-hPTH(1-3
245	18	52.9	36	15	AAR58214	[Ala19]-hPTH(1-36)
246	18	52.9	36	15	AAR58215	[D-Glu19]-hPTH(1-3
247	18	52.9	36	15	AAR58216	[Ala21]-hPTH(1-36)
248	18	52.9	36	15	AAR58217	[Ala22]-hPTH(1-36)
249	18	52.9	36	15	AAR58218	[Gln26]-hPTH(1-36)
250	18	52.9	36	15	AAR58219	[Nle26]-hPTH(1-36)
251	18	52.9	36	15	AAR58220	[D-Lys26]-hPTH(1-3
252	18	52.9	36	15	AAR58171	[N-Me-Ser1]-hPTH(1
253	18	52.9	36	15	AAR58188	[Phe23]-hPTH(1-36)
254	18	52.9	37	12	AAR11882	Parathyroid hormon
255	18	52.9	37	13	AAR24778	hPTH(1-37)-amide/e
256	18	52.9	37	15	AAR58244	[Ala0]-hPTH(1-36)-
257	18	52.9	37	15	AAR58245	[Pro0]-hPTH(1-36)-
258	18	52.9	37	22	AAB86226	Human parathyroid
259	18	52.9	37	22	AAB86229	Human parathyroid
260	18	52.9	37	23	ABB82203	Human parathyroid
261	18	52.9	38	3	AAP20248	Parathyroid hormon
262	18	52.9	38	15	AAR58282	[Trp(SO2Pmc)23]-hP
263	18	52.9	38	15	AAR58283	[Trp(Pmc)23]-hPTH(
264	18	52.9	38	15	AAR58018	Isopropyl-[Lys(Iso
265	18	52.9	38	15	AAR58137	[Phe20]-hPTH(1-38)
266	18	52.9	38	15	AAR58138	[Ala21]-hPTH(1-38)
267	18	52.9	38	15	AAR58139	[Gly21]-hPTH(1-38)
268	18	52.9	38	15	AAR58140	[Phe21]-hPTH(1-38)
269	18	52.9	38	15	AAR58141	[Leu21]-hPTH(1-38)
270	18	52.9	38	15	AAR58142	[Asn21]-hPTH(1-38)
271	18	52.9	38	15	AAR58143	[Gln21]-hPTH(1-38)
272	18	52.9	38	15	AAR58144	[Ser21]-hPTH(1-38)
273	18	52.9	38	15	AAR58145	[Gly22]-hPTH(1-38)
274	18	52.9	38	15	AAR58146	[Leu22]-hPTH(1-38)
275	18	52.9	38	15	AAR58147	[His22]-hPTH(1-38)
276	18	52.9	38	15	AAR58148	[Ala22]-hPTH(1-38)
277	18	52.9	38	15	AAR58149	[Ile22]-hPTH(1-38)
278	18	52.9	38	15	AAR58150	[Val22]-hPTH(1-38)

279	18	52.9	38	15	AAR58151	[Ser22]-hPTH(1-38)
280	18	52.9	38	15	AAR58152	[Arg22]-hPTH(1-38)
281	18	52.9	38	15	AAR58153	[Arg26]-hPTH(1-38)
282	18	52.9	38	15	AAR58154	[Val27]-hPTH(1-38)
283	18	52.9	38	15	AAR58155	[Ile27]-hPTH(1-38)
284	18	52.9	38	15	AAR58156	[Leu27]-hPTH(1-38)
285	18	52.9	38	15	AAR58157	[Arg27]-hPTH(1-38)
286	18	52.9	38	15	AAR58158	[Ala27]-hPTH(1-38)
287	18	52.9	38	15	AAR58159	[Val28]-hPTH(1-38)
288	18	52.9	38	15	AAR58160	[Ile28]-hPTH(1-38)
289	18	52.9	38	15	AAR58162	[Arg33]-hPTH(1-38)
290	18	52.9	38	15	AAR58163	[Pro33]-hPTH(1-38)
291	18	52.9	38	15	AAR58164	[Asp33]-hPTH(1-38)
292	18	52.9	38	15	AAR58165	[Ile33]-hPTH(1-38)
293	18	52.9	38	15	AAR58166	[Lys33]-hPTH(1-38)
294	18	52.9	38	15	AAR58167	[Ile31,Arg33]-hPTH
295	18	52.9	38	15	AAR58075	[Ser33]-hPTH(1-38)
296	18	52.9	38	15	AAR58076	[Thr33]-hPTH(1-38)
297	18	52.9	38	15	AAR58077	[Leu33]-hPTH(1-38)
298	18	52.9	38	15	AAR58078	[Gly33]-hPTH(1-38)
299	18	52.9	38	15	AAR58084	[Gln33]-hPTH(1-38)
300	18	52.9	38	15	AAR58123	[Ser19]-hPTH(1-38)
301	18	52.9	38	15	AAR58124	[Lys19]-hPTH(1-38)
302	18	52.9	38	15	AAR58125	[Leu19]-hPTH(1-38)
303	18	52.9	38	15	AAR58126	[Ala19]-hPTH(1-38)
304	18	52.9	38	15	AAR58127	[Tyr19]-hPTH(1-38)
305	18	52.9	38	15	AAR58128	[Met19]-hPTH(1-38)
306	18	52.9	38	15	AAR58129	[His19]-hPTH(1-38)
307	18	52.9	38	15	AAR58130	[Val19]-hPTH(1-38)
308	18	52.9	38	15	AAR58131	[Gly19]-hPTH(1-38)
309	18	52.9	38	15	AAR58132	[Pro19]-hPTH(1-38)
310	18	52.9	38	15	AAR58133	[Asp19]-hPTH(1-38)
311	18	52.9	38	15	AAR58134	[Ile19]-hPTH(1-38)
312	18	52.9	38	15	AAR58135	[Val19,Gln24]-hPTH
313	18	52.9	38	15	AAR54234	PTH N-terminal. S
314	18	52.9	38	20	AAAY02580	N-terminal 38 resi
315	18	52.9	38	22	AAB91101	Parathyroid hormon
316	18	52.9	38	23	AAE23729	Human parathyroid
317	18	52.9	38	23	AAE18400	Human PTH peptide
318	18	52.9	38	23	AAU73026	Parathyroid hormon
319	17	50.0	28	21	AAAY98041	Human parathyroid
320	17	50.0	28	21	AAAY98048	Human parathyroid
321	17	50.0	28	21	AAAY98050	Human parathyroid
322	17	50.0	30	23	AAU73055	Parathyroid hormon
323	17	50.0	33	21	AAAY98012	Human amino-termin
324	17	50.0	33	21	AAAY98015	Human amino-termin
325	17	50.0	34	13	AAR22291	Human parathyroid
326	17	50.0	34	19	AAW67298	Parathyroid hormon
327	17	50.0	34	19	AAW67300	Parathyroid hormon
328	17	50.0	34	19	AAW67301	Parathyroid hormon
329	17	50.0	34	21	ABJ10742	Human parathyroid
330	17	50.0	34	21	AAAY98010	Human amino-termin
331	17	50.0	34	21	AAAY98011	Human amino-termin
332	17	50.0	34	21	AAAY98014	Human amino-termin
333	17	50.0	34	22	AAB91087	Parathyroid hormon
334	17	50.0	34	22	AAB91113	Parathyroid hormon
335	17	50.0	34	23	AAE23728	Human parathyroid

336	17	50.0	34	23	AAE18399	Human PTH peptide
337	17	50.0	34	23	AAU73032	Parathyroid hormon
338	17	50.0	36	12	AAR15842	Human parathyroid
339	17	50.0	36	13	AAR23995	Human paprthyroid
340	17	50.0	36	15	AAR58254	[4-aminosalicylic
341	17	50.0	36	15	AAR58255	[TMSA1]-hPTH(1-36)
342	17	50.0	36	15	AAR58256	[Phe1]-hPTH(1-36) -
343	17	50.0	36	15	AAR58257	[Propargylglycin1]
344	17	50.0	36	15	AAR58262	[Ala1]-hPTH(1-36) -
345	17	50.0	36	15	AAR58277	[Nle18]-hPTH(1-36)
346	17	50.0	36	15	AAR58243	Propargyl-[Al1]-hPT
347	17	50.0	36	15	AAR58247	[Hyp1]-hPTH(1-36) -
348	17	50.0	36	15	AAR58248	N-Dimethyl-[Ala1]-
349	17	50.0	36	15	AAR58250	[Lys(For)1]-hPTH(1
350	17	50.0	36	15	AAR58251	[D-glyceric acid1]
351	17	50.0	36	15	AAR58252	[Asn1]-hPTH(1-36) -
352	17	50.0	36	15	AAR58253	[4-aminobenzoic ac
353	17	50.0	36	15	AAR58169	[D-Prol]-hPTH(1-36
354	17	50.0	36	15	AAR58170	[Nva1]-hPTH(1-36) -
355	17	50.0	36	15	AAR58172	[Indole-2-carboxyl
356	17	50.0	36	15	AAR58173	[Indole-3-carboxyl
357	17	50.0	36	15	AAR58174	[Pyridine-3-carbox
358	17	50.0	36	15	AAR58175	[Pyridine-2-carbox
359	17	50.0	36	15	AAR58176	[Hexahydropyridazi
360	17	50.0	36	15	AAR58177	[Morpholine-2-carb
361	17	50.0	36	15	AAR58178	[Prol]-hPTH(1-36) -
362	17	50.0	36	15	AAR58179	[Leu1]-hPTH(1-36) -
363	17	50.0	36	15	AAR58180	[Ile1]-hPTH(1-36) -
364	17	50.0	36	15	AAR58183	[Gln18]-hPTH(1-36)
365	17	50.0	36	15	AAR58184	[Tyr18]-hPTH(1-36)
366	17	50.0	36	15	AAR58185	[Lys18]-hPTH(1-36)
367	17	50.0	36	15	AAR58186	[Ala18]-hPTH(1-36)
368	17	50.0	36	15	AAR58026	N-alpha-methyl [Ala
369	17	50.0	36	15	AAR58168	[1-amino-cyclopent
370	17	50.0	37	23	AAU73027	Parathyroid hormon
371	17	50.0	38	15	AAR58019	N-alpha-methyl [Ala
372	17	50.0	38	15	AAR58022	[Ile1]-hPTH(1-38) -
373	17	50.0	38	15	AAR58028	[Thr1]-hPTH(1-38) -
374	17	50.0	38	15	AAR58029	[Leu1]-hPTH(1-38) -
375	17	50.0	38	15	AAR58030	[Abu1 or Gab1]-hP
376	16	47.1	28	22	AAB81078	Human parathyroid
377	16	47.1	31	22	AAB81077	Human parathyroid
378	16	47.1	32	5	AAP40427	Parathyroid antago
379	16	47.1	34	17	AAW14310	Cyclic parathyroid
380	16	47.1	34	17	AAW14311	Cyclic parathyroid
381	16	47.1	34	18	AAW17958	Human parathyroid
382	16	47.1	34	22	AAB61638	Peptide #1 that ca
383	16	47.1	36	15	AAR58259	[aBU2]-hPTH(1-36) -
384	16	47.1	36	15	AAR58261	[Tert. Leu]-hPTH(1-
385	16	47.1	36	15	AAR58212	[Ala17]-hPTH(1-36)
386	16	47.1	36	15	AAR58041	[L8, D10, K11, S14, I1
387	16	47.1	36	15	AAR58043	[L8, Q16, D17, L18, R1
388	16	47.1	38	15	AAR58023	[Ala1, Abu2 or Nva2
389	16	47.1	38	15	AAR58024	[Ala1, Ile2]-hPTH(1
390	16	47.1	38	15	AAR58120	[Ala17]-hPTH(1-38)
391	16	47.1	38	15	AAR58121	[Met17]-hPTH(1-38)
392	16	47.1	38	15	AAR58122	[Ile17]-hPTH(1-38)

393	15	44.1	28	13	AAR22058	Modified bovine PT
394	15	44.1	28	13	AAR22064	Modified hPTH(7-34
395	15	44.1	28	21	ABJ10775	Human parathyroid
396	15	44.1	28	21	ABJ10776	Human parathyroid
397	15	44.1	28	23	AAE23734	Human parathyroid
398	15	44.1	28	23	AAU73044	Parathyroid hormon
399	15	44.1	28	23	AAU73046	Parathyroid hormon
400	15	44.1	30	23	AAE23752	Human parathyroid
401	15	44.1	30	23	AAU73059	Parathyroid hormon
402	15	44.1	31	5	AAP40760	Human parathyroid
403	15	44.1	32	21	AAB07468	Antigenic peptide
404	15	44.1	32	22	AAB91096	Parathyroid hormon
405	15	44.1	32	23	AAE23735	Human parathyroid
406	15	44.1	32	23	AAE23739	Bovine parathyroid
407	15	44.1	32	23	AAE18402	Bovine PTH peptide
408	15	44.1	32	23	AAU73042	Parathyroid hormon
409	15	44.1	34	11	AAR07918	Bovine parathyroid
410	15	44.1	34	11	AAR08299	Bovine parathyroid
411	15	44.1	34	11	AAR08300	Human parathyroid
412	15	44.1	34	13	AAR22292	Human parathyroid
413	15	44.1	34	13	AAR22293	Human parathyroid
414	15	44.1	34	13	AAR22294	Human parathyroid
415	15	44.1	34	13	AAR22295	Human parathyroid
416	15	44.1	34	13	AAR22296	Human parathyroid
417	15	44.1	34	14	AAR41550	[D-Ala3]hPTH (1-34
418	15	44.1	34	14	AAR41551	[Thr16]hPTH (1-34)
419	15	44.1	34	14	AAR41552	[Glu16]hPTH (1-34)
420	15	44.1	34	14	AAR41553	[Lys16]hPTH (1-34)
421	15	44.1	34	14	AAR41561	[Lys16, Gln27]hPTH
422	15	44.1	34	14	AAR41562	[Orn16, Gln27]hPTH
423	15	44.1	34	14	AAR41563	[Hci16, Gln27]hPTH
424	15	44.1	34	14	AAR41564	[Asp16, Gln27]hPTH
425	15	44.1	34	14	AAR41565	[Arg16, Gln27]hPTH
426	15	44.1	34	14	AAR41571	[D-Lys16]hPTH (1-3
427	15	44.1	34	14	AAR41573	[Gln16]hPTH (1-34)
428	15	44.1	34	14	AAR41574	[Ser16]hPTH (1-34)
429	15	44.1	34	14	AAR41575	[Gly16]hPTH (1-34)
430	15	44.1	34	14	AAR41576	[Lys16]hPTH (1-34)
431	15	44.1	34	14	AAR41577	[Lys16, Asp17]hPTH
432	15	44.1	34	14	AAR41578	[Lys14,15,16,17]hP
433	15	44.1	34	14	AAR41579	[Lys15,15,17]hPTH
434	15	44.1	34	14	AAR41580	[Lys16,17]hPTH (1-
435	15	44.1	34	14	AAR41581	[Arg16,17]hPTH (1-
436	15	44.1	34	14	AAR41582	[Arg15,16,17]hPTH
437	15	44.1	34	15	AAR49697	Sequence of varian
438	15	44.1	34	15	AAR49698	Sequence of varian
439	15	44.1	34	15	AAR58239	Isopropyl- [Nle8,18
440	15	44.1	34	15	AAR58241	[Nle8,18,D-Asn33,D
441	15	44.1	34	17	AAW15812	[Trp(10)]-hPTH(1-3
442	15	44.1	34	17	AAW14308	Cyclic parathyroid
443	15	44.1	34	17	AAW14309	Cyclic parathyroid
444	15	44.1	34	17	AAW14312	Cyclic parathyroid
445	15	44.1	34	17	AAW14313	Cyclic parathyroid
446	15	44.1	34	17	AAW14314	Cyclic parathyroid
447	15	44.1	34	17	AAW14315	Cyclic parathyroid
448	15	44.1	34	17	AAW14316	Cyclic parathyroid
449	15	44.1	34	17	AAR99979	Bovine parathyroid

450	15	44.1	34	17	AAR99981	Porcine parathyroi
451	15	44.1	34	18	AAW08120	Human PTH derivati
452	15	44.1	34	18	AAW08121	Human PTH derivati
453	15	44.1	34	18	AAW08122	Human PTH derivati
454	15	44.1	34	18	AAW08123	Human PTH derivati
455	15	44.1	34	18	AAW08124	Human PTH derivati
456	15	44.1	34	18	AAW08129	Human PTH derivati
457	15	44.1	34	18	AAW08108	Human parathyroid
458	15	44.1	34	18	AAW08109	Human parathyroid
459	15	44.1	34	18	AAW08111	Human PTH derivati
460	15	44.1	34	18	AAW08112	Human PTH derivati
461	15	44.1	34	18	AAW08113	Human PTH derivati
462	15	44.1	34	18	AAW08114	Human PTH derivati
463	15	44.1	34	18	AAW08115	Human PTH derivati
464	15	44.1	34	18	AAW08116	Human PTH derivati
465	15	44.1	34	18	AAW08117	Human PTH derivati
466	15	44.1	34	18	AAW08118	Human PTH derivati
467	15	44.1	34	18	AAW08119	Human PTH derivati
468	15	44.1	34	18	AAW19995	Cyclised bovine pa
469	15	44.1	34	18	AAW20001	Cyclised bovine pa
470	15	44.1	34	18	AAW20007	Cyclised bovine pa
471	15	44.1	34	18	AAW17941	Human parathyroid
472	15	44.1	34	18	AAW17942	Human parathyroid
473	15	44.1	34	18	AAW17943	Human parathyroid
474	15	44.1	34	18	AAW17967	Human PTH analogue
475	15	44.1	34	18	AAW17939	Human parathyroid
476	15	44.1	34	18	AAW17952	Human parathyroid
477	15	44.1	34	18	AAW17953	Human parathyroid
478	15	44.1	34	18	AAW17956	Human parathyroid
479	15	44.1	34	18	AAW17957	Human parathyroid
480	15	44.1	34	18	AAW17959	Human parathyroid
481	15	44.1	34	18	AAW17962	Human PTH analogue
482	15	44.1	34	18	AAW17963	Human PTH analogue
483	15	44.1	34	18	AAW01609	Parathryoid hormon
484	15	44.1	34	19	AAW67274	Parathyroid hormon
485	15	44.1	34	19	AAW67276	Parathyroid hormon
486	15	44.1	34	19	AAW67277	Parathyroid hormon
487	15	44.1	34	19	AAW67278	Parathyroid hormon
488	15	44.1	34	19	AAW67287	Parathyroid hormon
489	15	44.1	34	19	AAW67290	Parathyroid hormon
490	15	44.1	34	19	AAW67299	Parathyroid hormon
491	15	44.1	34	19	AAW61659	Parathyroid hormon
492	15	44.1	34	19	AAW61660	Parathyroid hormon
493	15	44.1	34	19	AAW65976	Bovine parathyroid
494	15	44.1	34	19	AAW65977	Porcine parathyroi
495	15	44.1	34	19	AAW42615	Bovine parathyroid
496	15	44.1	34	19	AAW42616	Porcine parathyroi
497	15	44.1	34	20	AAW92218	Analogue of parath
498	15	44.1	34	20	AAW92219	Analogue of parath
499	15	44.1	34	20	AAW03920	Analogue of parath
500	15	44.1	34	20	AAW03921	Analogue of parath
501	15	44.1	34	20	AAW03922	Analogue of parath
502	15	44.1	34	20	AAW03923	Analogue of parath
503	15	44.1	34	20	AAW03924	Analogue of parath
504	15	44.1	34	20	AAW03925	Analogue of parath
505	15	44.1	34	20	AAW03926	Analogue of parath
506	15	44.1	34	20	AAW03927	Analogue of parath

507	15	44.1	34	20	AAAY03928	Analogue of parath
508	15	44.1	34	20	AAAY03929	Analogue of parath
509	15	44.1	34	20	AAAY03930	Analogue of parath
510	15	44.1	34	20	AAAY03931	Analogue of parath
511	15	44.1	34	20	AAAY03932	Analogue of parath
512	15	44.1	34	20	AAAY03933	Analogue of parath
513	15	44.1	34	20	AAW92236	Analogue of parath
514	15	44.1	34	20	AAW92237	Analogue of parath
515	15	44.1	34	20	AAW92238	Analogue of parath
516	15	44.1	34	20	AAW92239	Analogue of parath
517	15	44.1	34	20	AAW92240	Analogue of parath
518	15	44.1	34	20	AAW92241	Analogue of parath
519	15	44.1	34	20	AAW92242	Analogue of parath
520	15	44.1	34	20	AAW92243	Analogue of parath
521	15	44.1	34	20	AAW92244	Analogue of parath
522	15	44.1	34	20	AAW92245	Analogue of parath
523	15	44.1	34	20	AAW92246	Analogue of parath
524	15	44.1	34	20	AAW92247	Analogue of parath
525	15	44.1	34	20	AAW92248	Analogue of parath
526	15	44.1	34	20	AAW92249	Analogue of parath
527	15	44.1	34	20	AAW92250	Analogue of parath
528	15	44.1	34	20	AAAY03919	Analogue of parath
529	15	44.1	34	20	AAW92220	Analogue of parath
530	15	44.1	34	20	AAW92221	Analogue of parath
531	15	44.1	34	20	AAW92222	Analogue of parath
532	15	44.1	34	20	AAW92223	Analogue of parath
533	15	44.1	34	20	AAW92224	Analogue of parath
534	15	44.1	34	20	AAW92225	Analogue of parath
535	15	44.1	34	20	AAW92226	Analogue of parath
536	15	44.1	34	20	AAW92227	Analogue of parath
537	15	44.1	34	20	AAW92228	Analogue of parath
538	15	44.1	34	20	AAW92229	Analogue of parath
539	15	44.1	34	20	AAW92230	Analogue of parath
540	15	44.1	34	20	AAW92231	Analogue of parath
541	15	44.1	34	20	AAW92232	Analogue of parath
542	15	44.1	34	20	AAW92233	Analogue of parath
543	15	44.1	34	20	AAW92234	Analogue of parath
544	15	44.1	34	20	AAW92235	Analogue of parath
545	15	44.1	34	20	AAAY03947	Analogue of parath
546	15	44.1	34	20	AAAY03948	Analogue of parath
547	15	44.1	34	20	AAW92204	Analogue of parath
548	15	44.1	34	20	AAW92205	Analogue of parath
549	15	44.1	34	20	AAW92207	Analogue of parath
550	15	44.1	34	20	AAW92208	Analogue of parath
551	15	44.1	34	20	AAW92209	Analogue of parath
552	15	44.1	34	20	AAW92210	Analogue of parath
553	15	44.1	34	20	AAW92211	Analogue of parath
554	15	44.1	34	20	AAW92212	Analogue of parath
555	15	44.1	34	20	AAW92213	Analogue of parath
556	15	44.1	34	20	AAW92214	Analogue of parath
557	15	44.1	34	20	AAW92215	Analogue of parath
558	15	44.1	34	20	AAW92216	Analogue of parath
559	15	44.1	34	20	AAW92217	Analogue of parath
560	15	44.1	34	20	AAW92206	Analogue of parath
561	15	44.1	34	20	AAW92203	Analogue of parath
562	15	44.1	34	20	AAAY03934	Analogue of parath
563	15	44.1	34	20	AAAY03935	Analogue of parath

564	15	44.1	34	20	AAAY03936	Analogue of parath
565	15	44.1	34	20	AAAY03937	Analogue of parath
566	15	44.1	34	20	AAAY03938	Analogue of parath
567	15	44.1	34	20	AAAY03939	Analogue of parath
568	15	44.1	34	20	AAAY03940	Analogue of parath
569	15	44.1	34	20	AAAY03941	Analogue of parath
570	15	44.1	34	20	AAAY03942	Analogue of parath
571	15	44.1	34	20	AAAY03943	Analogue of parath
572	15	44.1	34	20	AAAY03944	Analogue of parath
573	15	44.1	34	20	AAAY03945	Analogue of parath
574	15	44.1	34	20	AAAY03946	Analogue of parath
575	15	44.1	34	20	AAAY03949	Analogue of parath
576	15	44.1	34	20	AAAY03950	Analogue of parath
577	15	44.1	34	20	AAAY03951	Analogue of parath
578	15	44.1	34	20	AAAY03952	Analogue of parath
579	15	44.1	34	20	AAAY03953	Analogue of parath
580	15	44.1	34	20	AAAY03954	Analogue of parath
581	15	44.1	34	20	AAAY03955	Analogue of parath
582	15	44.1	34	20	AAAY03956	Analogue of parath
583	15	44.1	34	20	AAW92198	Analogue of parath
584	15	44.1	34	20	AAW92199	Analogue of parath
585	15	44.1	34	20	AAW92200	Analogue of parath
586	15	44.1	34	20	AAW92201	Analogue of parath
587	15	44.1	34	20	AAW92202	Analogue of parath
588	15	44.1	34	20	AAW92183	Analogue of parath
589	15	44.1	34	20	AAW92184	Analogue of parath
590	15	44.1	34	20	AAW92185	Analogue of parath
591	15	44.1	34	20	AAW92186	Analogue of parath
592	15	44.1	34	20	AAW92187	Analogue of parath
593	15	44.1	34	20	AAW92167	Analogue of parath
594	15	44.1	34	20	AAW92188	Analogue of parath
595	15	44.1	34	20	AAW92189	Analogue of parath
596	15	44.1	34	20	AAW92190	Analogue of parath
597	15	44.1	34	20	AAW92191	Analogue of parath
598	15	44.1	34	20	AAW92192	Analogue of parath
599	15	44.1	34	20	AAW92193	Analogue of parath
600	15	44.1	34	20	AAW92194	Analogue of parath
601	15	44.1	34	20	AAW92195	Analogue of parath
602	15	44.1	34	20	AAW92196	Analogue of parath
603	15	44.1	34	20	AAW92197	Analogue of parath
604	15	44.1	34	20	AAW92166	Analogue of parath
605	15	44.1	34	20	AAW92168	Analogue of parath
606	15	44.1	34	20	AAW92169	Analogue of parath
607	15	44.1	34	20	AAW92170	Analogue of parath
608	15	44.1	34	20	AAW92171	Analogue of parath
609	15	44.1	34	20	AAW92172	Analogue of parath
610	15	44.1	34	20	AAW92173	Analogue of parath
611	15	44.1	34	20	AAW92174	Analogue of parath
612	15	44.1	34	20	AAW92175	Analogue of parath
613	15	44.1	34	20	AAW92176	Analogue of parath
614	15	44.1	34	20	AAW92177	Analogue of parath
615	15	44.1	34	20	AAW92178	Analogue of parath
616	15	44.1	34	20	AAW92179	Analogue of parath
617	15	44.1	34	20	AAW92180	Analogue of parath
618	15	44.1	34	20	AAW92181	Analogue of parath
619	15	44.1	34	20	AAW92182	Analogue of parath
620	15	44.1	34	20	AAW92152	Analogue of parath

621	15	44.1	34	20	AAW92150	Analogue of parath
622	15	44.1	34	20	AAW92151	Analogue of parath
623	15	44.1	34	20	AAW92153	Analogue of parath
624	15	44.1	34	20	AAW92154	Analogue of parath
625	15	44.1	34	20	AAW92155	Analogue of parath
626	15	44.1	34	20	AAW92156	Analogue of parath
627	15	44.1	34	20	AAW92157	Analogue of parath
628	15	44.1	34	20	AAW92158	Analogue of parath
629	15	44.1	34	20	AAW92159	Analogue of parath
630	15	44.1	34	20	AAW92160	Analogue of parath
631	15	44.1	34	20	AAW92161	Analogue of parath
632	15	44.1	34	20	AAW92162	Analogue of parath
633	15	44.1	34	20	AAW92163	Analogue of parath
634	15	44.1	34	20	AAW92164	Analogue of parath
635	15	44.1	34	20	AAW92165	Analogue of parath
636	15	44.1	34	20	AAW92148	Analogue of parath
637	15	44.1	34	20	AAW92149	Analogue of parath
638	15	44.1	34	20	AAW81872	Bovine PTH N-termi
639	15	44.1	34	20	AAW81873	Porcine PTH N-term
640	15	44.1	34	21	ABJ10706	Human parathyroid
641	15	44.1	34	21	ABJ10713	Human parathyroid
642	15	44.1	34	21	ABJ10714	Human parathyroid
643	15	44.1	34	21	ABJ10717	Human parathyroid
644	15	44.1	34	21	ABJ10719	Human parathyroid
645	15	44.1	34	21	ABJ10722	Human parathyroid
646	15	44.1	34	21	ABJ10724	Human parathyroid
647	15	44.1	34	21	ABJ10727	Human parathyroid
648	15	44.1	34	21	ABJ10729	Human parathyroid
649	15	44.1	34	21	ABJ10730	Human parathyroid
650	15	44.1	34	21	ABJ10733	Human parathyroid
651	15	44.1	34	21	ABJ10735	Human parathyroid
652	15	44.1	34	21	ABJ10736	Human parathyroid
653	15	44.1	34	21	ABJ10737	Human parathyroid
654	15	44.1	34	21	ABJ10739	Human parathyroid
655	15	44.1	34	21	ABJ10740	Human parathyroid
656	15	44.1	34	21	ABJ10743	Human parathyroid
657	15	44.1	34	21	ABJ10769	Human parathyroid
658	15	44.1	34	21	ABJ10770	Human parathyroid
659	15	44.1	34	22	AAB91084	Parathyroid hormon
660	15	44.1	34	23	AAE23738	Bovine parathyroid
661	15	44.1	34	23	AAE18394	Bovine PTH peptide
662	15	44.1	34	23	AAU73029	Parathyroid hormon
663	15	44.1	34	23	AAU73030	Parathyroid hormon
664	15	44.1	34	23	AAU73034	Parathyroid hormon
665	15	44.1	34	23	AAU73036	Parathyroid hormon
666	15	44.1	35	2	AAP10140	h-PTH antigen. Sy
667	15	44.1	35	16	AAR74401	Parathyroid hormon
668	15	44.1	35	16	AAR74412	Parathyroid hormon
669	15	44.1	35	23	AAU73173	Parathyroid hormon
670	15	44.1	36	15	AAR58266	[Nle8]-hPTH(1-36) -
671	15	44.1	36	15	AAR58267	[Phe8]-hPTH(1-36) -
672	15	44.1	36	15	AAR58268	[Cha8]-hPTH(1-36) -
673	15	44.1	36	15	AAR58271	[Ala11]-hPTH(1-36)
674	15	44.1	36	15	AAR58274	[Ala15]-hPTH(1-36)
675	15	44.1	36	15	AAR58275	[Ala16]-hPTH(1-36)
676	15	44.1	36	15	AAR58197	[Ala3]-hPTH(1-36) -
677	15	44.1	36	15	AAR58201	[Ala10]-hPTH(1-36)

678	15	44.1	36	15	AAR58203	[Ala12]-hPTH(1-36)
679	15	44.1	36	15	AAR58204	[Gln13]-hPTH(1-36)
680	15	44.1	36	15	AAR58205	[His13]-hPTH(1-36)
681	15	44.1	36	15	AAR58206	[Leu13]-hPTH(1-36)
682	15	44.1	36	15	AAR58207	[Ala13]-hPTH(1-36)
683	15	44.1	36	15	AAR58209	[Ala14]-hPTH(1-36)
684	15	44.1	36	15	AAR58182	[Nva8]-hPTH(1-36)-
685	15	44.1	36	15	AAR58042	[L8,D10,K11,L18]-h
686	15	44.1	36	15	AAR58044	[L8,D10,K11,A17,L1
687	15	44.1	36	15	AAR58046	[L8,A16,D17,L18,A1
688	15	44.1	36	15	AAR58047	[L8,D10,A16,D17,L1
689	15	44.1	36	15	AAR58050	[L8,A16,D17,Q18,A1
690	15	44.1	36	15	AAR58051	[L8,A16,A17,Q18,A1
691	15	44.1	36	15	AAR58052	[L8,A17,Q18,A19]-h
692	15	44.1	36	15	AAR58055	[L8,Q18]-hPTH(1-36
693	15	44.1	36	15	AAR58057	[L8,D10,A16,Q18]-h
694	15	44.1	36	15	AAR58067	[L8,A16,A17,A18,A1
695	15	44.1	36	15	AAR58069	Isopropyl-[L8,K(Is
696	15	44.1	36	15	AAR58070	Isopropyl-[L8,K(Is
697	15	44.1	36	15	AAR58071	[Aib3,Gln18]-hPTH
698	15	44.1	36	15	AAR55820	[L8,D10,K11,Q18]-h
699	15	44.1	36	15	AAR55822	[L8,D10,K11,A16,Q1
700	15	44.1	36	15	AAR55824	[L8,D10,K11,A16,Q1
701	15	44.1	36	15	AAR55825	[L8,A16,Q18,A19]-h
702	15	44.1	36	15	AAR58027	[A1,A3,L8,Q18]-hPT
703	15	44.1	36	15	AAR58031	[L8,K11,Q18]-hPTH(
704	15	44.1	36	15	AAR58072	Isopropyl-[L8,D10,
705	15	44.1	36	15	AAR58074	[L8,Y18]-hPTH(1-36
706	15	44.1	36	15	AAR58086	[1-amino-cyclopent
707	15	44.1	36	15	AAR58088	[1-amino-cyclopent
708	15	44.1	37	22	AAB86230	Bovine parathyroid
709	15	44.1	37	22	AAB86232	Porcine parathyroi
710	15	44.1	37	22	AAB86233	Canine parathyroid
711	15	44.1	37	23	ABB82204	Bovine parathyroid
712	15	44.1	38	15	AAR58269	[Leu8]-hPTH(1-38)-
713	15	44.1	38	15	AAR58061	[Ile15]-hPTH(1-38)
714	15	44.1	38	15	AAR58036	[Gln16]-hPTH(1-38)
715	15	44.1	38	15	AAR58037	[Ser14]-hPTH(1-38)
716	15	44.1	38	15	AAR58161	[Pro3,Thr33]-hPTH(
717	15	44.1	38	15	AAR58089	[Arg12]-hPTH(1-38)
718	15	44.1	38	15	AAR58090	[Ser12]-hPTH(1-38)
719	15	44.1	38	15	AAR58091	[Cys13]-hPTH(1-38)
720	15	44.1	38	15	AAR58092	[Ile13]-hPTH(1-38)
721	15	44.1	38	15	AAR58093	[Asn13]-hPTH(1-38)
722	15	44.1	38	15	AAR58094	[Trp13]-hPTH(1-38)
723	15	44.1	38	15	AAR58095	[Asp13]-hPTH(1-38)
724	15	44.1	38	15	AAR58096	[Val13]-hPTH(1-38)
725	15	44.1	38	15	AAR58097	[Thr13]-hPTH(1-38)
726	15	44.1	38	15	AAR58098	[Ser13]-hPTH(1-38)
727	15	44.1	38	15	AAR58099	[Tyr13]-hPTH(1-38)
728	15	44.1	38	15	AAR58100	[Met13]-hPTH(1-38)
729	15	44.1	38	15	AAR58101	[Gln13]-hPTH(1-38)
730	15	44.1	38	15	AAR58102	[Leu13]-hPTH(1-38)
731	15	44.1	38	15	AAR58103	[Ala13]-hPTH(1-38)
732	15	44.1	38	15	AAR58104	[Gly13]-hPTH(1-38)
733	15	44.1	38	15	AAR58105	[Val14]-hPTH(1-38)
734	15	44.1	38	15	AAR58106	[Ala14]-hPTH(1-38)

735	15	44.1	38	15	AAR58107	[Lys14]-hPTH(1-38)
736	15	44.1	38	15	AAR58108	[Arg14]-hPTH(1-38)
737	15	44.1	38	15	AAR58109	[Thr14]-hPTH(1-38)
738	15	44.1	38	15	AAR58110	[Ile14]-hPTH(1-38)
739	15	44.1	38	15	AAR58111	[Tyr14]-hPTH(1-38)
740	15	44.1	38	15	AAR58112	[Tyr15]-hPTH(1-38)
741	15	44.1	38	15	AAR58113	[Arg15]-hPTH(1-38)
742	15	44.1	38	15	AAR58114	[Val15]-hPTH(1-38)
743	15	44.1	38	15	AAR58115	[Lys16]-hPTH(1-38)
744	15	44.1	38	15	AAR58116	[Ser16]-hPTH(1-38)
745	15	44.1	38	15	AAR58117	[Leu16]-hPTH(1-38)
746	15	44.1	38	15	AAR58118	[Ala16]-hPTH(1-38)
747	15	44.1	38	15	AAR58119	[Gly16]-hPTH(1-38)
748	15	44.1	38	17	AAR98958	Target peptide (PT
749	14	41.2	28	13	AAR22059	Modified [Tyr_34]b
750	14	41.2	28	13	AAR22060	Modified [D-Trp_12
751	14	41.2	28	13	AAR22061	Modified [Nle_8,18
752	14	41.2	28	13	AAR22062	Modified [Nle_8,18
753	14	41.2	28	13	AAR22065	Modified [Tyr_34]h
754	14	41.2	28	13	AAR22066	Modified [D-Trp_12
755	14	41.2	28	13	AAR22067	Modified [Nle_8,_1
756	14	41.2	28	13	AAR22068	Modified [Nle_8,_1
757	14	41.2	28	21	ABJ10774	Human parathyroid
758	14	41.2	28	22	AAB91115	Parathyroid hormon
759	14	41.2	28	23	AAE18404	Bovine PTH peptide
760	14	41.2	28	23	AAE18405	Bovine PTH peptide
761	14	41.2	28	23	AAU73045	Parathyroid hormon
762	14	41.2	28	23	AAU73047	Parathyroid hormon
763	14	41.2	28	23	AAU73048	Parathyroid hormon
764	14	41.2	28	23	AAU73049	Parathyroid hormon
765	14	41.2	28	23	AAU73050	Parathyroid hormon
766	14	41.2	30	6	AAP50665	Human parathyroid
767	14	41.2	30	22	AAB91089	Parathyroid hormon
768	14	41.2	30	22	AAB91092	Parathyroid hormon
769	14	41.2	30	23	AAU73060	Parathyroid hormon
770	14	41.2	31	5	AAP40510	Bovine parathyroid
771	14	41.2	31	5	AAP40511	Bovine parathyroid
772	14	41.2	31	5	AAP40761	Human parathyroid
773	14	41.2	32	22	AAB91088	Parathyroid hormon
774	14	41.2	32	22	AAB91090	Parathyroid hormon
775	14	41.2	32	22	AAB91091	Parathyroid hormon
776	14	41.2	32	23	AAE18403	Bovine PTH peptide
777	14	41.2	32	23	AAU73041	Parathyroid hormon
778	14	41.2	32	23	AAU73043	Parathyroid hormon
779	14	41.2	33	17	AAR88841	Human parathyroid
780	14	41.2	34	6	AAP50517	Sequence of methio
781	14	41.2	34	9	AAP82177	Sequence of parath
782	14	41.2	34	11	AAR07917	Rat parathyroid ho
783	14	41.2	34	11	AAR07920	Rat parathyroid ho
784	14	41.2	34	11	AAR07921	Bovine parathyroid
785	14	41.2	34	11	AAR07924	Bovine parathyroid
786	14	41.2	34	11	AAR07925	Human parathyroid
787	14	41.2	34	11	AAR08302	Bovine parathyroid
788	14	41.2	34	11	AAR08303	Human parathyroid
789	14	41.2	34	11	AAR08305	Bovine parathyroid
790	14	41.2	34	11	AAR08306	Human parathyroid
791	14	41.2	34	14	AAR41568	[Lys15,16 His27]hP

792	14	41.2	34	14	AAR41569	[Lys15, His27]hPTH
793	14	41.2	34	14	AAR41572	[Lys15,16,17, His2
794	14	41.2	34	15	AAR45528	Parathyroid hormon
795	14	41.2	34	15	AAR58195	[S14,I15,Q16,D17,L
796	14	41.2	34	15	AAR58045	[L8,Q16,D17,L18,R1
797	14	41.2	34	15	AAR58049	[L8,D10,K11,Q16,D1
798	14	41.2	34	16	AAR69055	PTH analogue with
799	14	41.2	34	16	AAR62432	Accelerator peptid
800	14	41.2	34	17	AAR99980	Rat parathyroid ho
801	14	41.2	34	18	AAW13352	Truncated parathyr
802	14	41.2	34	18	AAW12651	Parathyroid hormon
803	14	41.2	34	18	AAW19996	Cyclised rat parat
804	14	41.2	34	18	AAW20004	Cyclised [Nle 8,18
805	14	41.2	34	18	AAW19997	Cyclised [Nle 8,18
806	14	41.2	34	18	AAW19998	Cyclised [Nle 8,18
807	14	41.2	34	18	AAW20002	Cyclised rat parat
808	14	41.2	34	18	AAW20003	Cyclised [Nle 8,18
809	14	41.2	34	18	AAW20008	Cyclised rat parat
810	14	41.2	34	18	AAW20009	Cyclised [Nle 8,18
811	14	41.2	34	18	AAW20010	Cyclised [Nle 8,18
812	14	41.2	34	18	AAW17940	Human PTH analogue
813	14	41.2	34	18	AAW17970	Human PTH analogue
814	14	41.2	34	18	AAW17964	Human PTH analogue
815	14	41.2	34	18	AAW17960	Human PTH analogue
816	14	41.2	34	19	AAW67275	Parathyroid hormon
817	14	41.2	34	19	AAW61725	Parathyroid hormon
818	14	41.2	34	19	AAW66053	Parathyroid hormon
819	14	41.2	34	19	AAW42602	Parathyroid hormon
820	14	41.2	34	19	AAW48394	Human PTH/PTHrP hy
821	14	41.2	34	19	AAW48395	Human PTH/PTHrP hy
822	14	41.2	34	19	AAW48398	Human PTH/PTHrP hy
823	14	41.2	34	20	AAW74396	Modified parathyro
824	14	41.2	34	20	AAW81945	Synthetic PTH and
825	14	41.2	34	21	ABJ10705	Human parathyroid
826	14	41.2	34	21	ABJ10707	Human parathyroid
827	14	41.2	34	21	ABJ10708	Human parathyroid
828	14	41.2	34	21	ABJ10709	Human parathyroid
829	14	41.2	34	21	ABJ10710	Human parathyroid
830	14	41.2	34	21	ABJ10711	Human parathyroid
831	14	41.2	34	21	ABJ10715	Human parathyroid
832	14	41.2	34	21	ABJ10716	Human parathyroid
833	14	41.2	34	21	ABJ10718	Human parathyroid
834	14	41.2	34	21	ABJ10720	Human parathyroid
835	14	41.2	34	21	ABJ10721	Human parathyroid
836	14	41.2	34	21	ABJ10723	Human parathyroid
837	14	41.2	34	21	ABJ10725	Human parathyroid
838	14	41.2	34	21	ABJ10726	Human parathyroid
839	14	41.2	34	21	ABJ10728	Human parathyroid
840	14	41.2	34	21	ABJ10731	Human parathyroid
841	14	41.2	34	21	ABJ10732	Human parathyroid
842	14	41.2	34	21	ABJ10734	Human parathyroid
843	14	41.2	34	21	ABJ10738	Human parathyroid
844	14	41.2	34	21	ABJ10741	Human parathyroid
845	14	41.2	34	21	ABJ10744	Human parathyroid
846	14	41.2	34	21	ABJ10745	Human parathyroid
847	14	41.2	34	21	ABJ10746	Human parathyroid
848	14	41.2	34	21	ABJ10747	Human parathyroid

849	14	41.2	34	21	ABJ10748	Human parathyroid
850	14	41.2	34	21	ABJ10749	Human parathyroid
851	14	41.2	34	21	ABJ10750	Human parathyroid
852	14	41.2	34	21	ABJ10751	Human parathyroid
853	14	41.2	34	21	ABJ10752	Human parathyroid
854	14	41.2	34	21	ABJ10753	Human parathyroid
855	14	41.2	34	21	ABJ10754	Human parathyroid
856	14	41.2	34	21	ABJ10755	Human parathyroid
857	14	41.2	34	21	ABJ10756	Human parathyroid
858	14	41.2	34	21	ABJ10757	Human parathyroid
859	14	41.2	34	21	ABJ10761	Human parathyroid
860	14	41.2	34	21	ABJ10762	Human parathyroid
861	14	41.2	34	21	ABJ10763	Human parathyroid
862	14	41.2	34	21	ABJ10764	Human parathyroid
863	14	41.2	34	21	ABJ10765	Human parathyroid
864	14	41.2	34	21	ABJ10766	Human parathyroid
865	14	41.2	34	21	ABJ10767	Human parathyroid
866	14	41.2	34	21	ABJ10768	Human parathyroid
867	14	41.2	34	21	ABJ10771	Human parathyroid
868	14	41.2	34	21	ABJ10772	Human parathyroid
869	14	41.2	34	21	ABJ10773	Human parathyroid
870	14	41.2	34	21	ABJ10777	Human parathyroid
871	14	41.2	34	22	AAB84777	Native human parat
872	14	41.2	34	22	AAB96893	Rat parathyroid ho
873	14	41.2	34	22	AAB96897	Rat parathyroid ho
874	14	41.2	34	22	AAB96930	Rat parathyroid ho
875	14	41.2	34	22	AAB91100	Parathyroid hormon
876	14	41.2	34	23	AAE18396	Bovine PTH peptide
877	14	41.2	34	23	AAE18397	Human PTH peptide
878	14	41.2	34	23	AAU73033	Parathyroid hormon
879	14	41.2	34	23	AAU73035	Parathyroid hormon
880	14	41.2	34	23	AAU73037	Parathyroid hormon
881	14	41.2	34	24	ABP71489	Parathyroid hormon
882	14	41.2	34	24	ABP71499	Rat parathyroid ho
883	14	41.2	35	16	AAR74518	Parathyroid hormon
884	14	41.2	35	16	AAR74519	Parathyroid hormon
885	14	41.2	35	16	AAR74520	Parathyroid hormon
886	14	41.2	35	16	AAR74527	Human parathyroid
887	14	41.2	35	16	AAR74480	Parathyroid hormon
888	14	41.2	35	16	AAR74464	Parathyroid hormon
889	14	41.2	35	16	AAR74465	Parathyroid hormon
890	14	41.2	35	16	AAR74466	Parathyroid hormon
891	14	41.2	35	16	AAR74467	Parathyroid hormon
892	14	41.2	35	16	AAR74468	Parathyroid hormon
893	14	41.2	35	16	AAR74469	Parathyroid hormon
894	14	41.2	35	16	AAR74470	Parathyroid hormon
895	14	41.2	35	16	AAR74471	Parathyroid hormon
896	14	41.2	35	16	AAR74472	Parathyroid hormon
897	14	41.2	35	16	AAR74473	Parathyroid hormon
898	14	41.2	35	16	AAR74474	Parathyroid hormon
899	14	41.2	35	16	AAR74475	Parathyroid hormon
900	14	41.2	35	16	AAR74476	Parathyroid hormon
901	14	41.2	35	16	AAR74477	Parathyroid hormon
902	14	41.2	35	16	AAR74478	Parathyroid hormon
903	14	41.2	35	16	AAR74479	Parathyroid hormon
904	14	41.2	35	16	AAR74448	Parathyroid hormon
905	14	41.2	35	16	AAR74449	Parathyroid hormon

906	14	41.2	35	16	AAR74450	Parathyroid hormon
907	14	41.2	35	16	AAR74451	Parathyroid hormon
908	14	41.2	35	16	AAR74452	Parathyroid hormon
909	14	41.2	35	16	AAR74453	Parathyroid hormon
910	14	41.2	35	16	AAR74454	Parathyroid hormon
911	14	41.2	35	16	AAR74455	Parathyroid hormon
912	14	41.2	35	16	AAR74456	Parathyroid hormon
913	14	41.2	35	16	AAR74457	Parathyroid hormon
914	14	41.2	35	16	AAR74458	Parathyroid hormon
915	14	41.2	35	16	AAR74459	Parathyroid hormon
916	14	41.2	35	16	AAR74460	Parathyroid hormon
917	14	41.2	35	16	AAR74461	Parathyroid hormon
918	14	41.2	35	16	AAR74462	Parathyroid hormon
919	14	41.2	35	16	AAR74463	Parathyroid hormon
920	14	41.2	35	16	AAR74432	Parathyroid hormon
921	14	41.2	35	16	AAR74433	Parathyroid hormon
922	14	41.2	35	16	AAR74434	Parathyroid hormon
923	14	41.2	35	16	AAR74435	Parathyroid hormon
924	14	41.2	35	16	AAR74436	Parathyroid hormon
925	14	41.2	35	16	AAR74437	Parathyroid hormon
926	14	41.2	35	16	AAR74438	Parathyroid hormon
927	14	41.2	35	16	AAR74439	Parathyroid hormon
928	14	41.2	35	16	AAR74440	Parathyroid hormon
929	14	41.2	35	16	AAR74441	Parathyroid hormon
930	14	41.2	35	16	AAR74442	Parathyroid hormon
931	14	41.2	35	16	AAR74443	Parathyroid hormon
932	14	41.2	35	16	AAR74444	Parathyroid hormon
933	14	41.2	35	16	AAR74445	Parathyroid hormon
934	14	41.2	35	16	AAR74446	Parathyroid hormon
935	14	41.2	35	16	AAR74447	Parathyroid hormon
936	14	41.2	35	16	AAR74429	Parathyroid hormon
937	14	41.2	35	16	AAR74430	Parathyroid hormon
938	14	41.2	35	16	AAR74431	Parathyroid hormon
939	14	41.2	35	16	AAR74398	Parathyroid hormon
940	14	41.2	35	16	AAR74399	Parathyroid hormon
941	14	41.2	35	16	AAR74400	Parathyroid hormon
942	14	41.2	35	16	AAR74394	Parathyroid hormon
943	14	41.2	35	16	AAR74395	Parathyroid hormon
944	14	41.2	35	16	AAR74396	Parathyroid hormon
945	14	41.2	35	16	AAR74397	Parathyroid hormon
946	14	41.2	37	22	AAB86231	Rat parathyroid ho
947	13	38.2	32	17	AAR88840	Human parathyroid
948	13	38.2	32	22	AAB84835	Parathyroid hormon
949	13	38.2	32	22	AAB96906	Parathyroid hormon
950	13	38.2	33	17	AAW15814	[Leu(8), Trp(10), Al
951	13	38.2	34	15	AAR58193	[L8, D10, K11, T33, A3
952	13	38.2	34	15	AAR58194	[A1, H5, L8, D10, K11,
953	13	38.2	34	15	AAR58056	[L8, D10, K11, A16, Q1
954	13	38.2	34	15	AAR58058	[L8, D10, K11, A16, Q1
955	13	38.2	34	15	AAR55817	[L8, Q18, T33, A34] -h
956	13	38.2	34	15	AAR55818	[L8, A16, Q18, A19, T3
957	13	38.2	34	15	AAR55819	[L8, A16, Q18, T33, A3
958	13	38.2	34	15	AAR55821	[L8, D10, K11, Q18, T3
959	13	38.2	34	15	AAR55823	[L8, D10, K11, A16, Q1
960	13	38.2	34	15	AAR58021	[L8, D10, A16, Q18, T3
961	13	38.2	34	15	AAR58034	Isopropyl - [L8, K(Is
962	13	38.2	34	17	AAW15813	[Leu(8), Trp(10), Al

963	13	38.2	34	17	AAW15815	[Leu(8),Trp(10),DL
964	13	38.2	34	17	AAW15828	N-alpha-acylated [
965	13	38.2	34	18	AAW08131	Human PTH derivati
966	13	38.2	34	20	AAV02587	Parathyroid hormon
967	13	38.2	34	21	ABJ10758	Human parathyroid
968	13	38.2	34	22	AAB84771	Parathyroid hormon
969	13	38.2	34	22	AAB84775	Parathyroid hormon
970	13	38.2	34	22	AAB84826	Parathyroid hormon
971	13	38.2	34	22	AAB96916	Parathyroid hormon
972	13	38.2	34	22	AAB96919	Parathyroid hormon
973	13	38.2	34	22	AAB96922	Parathyroid hormon
974	13	38.2	34	22	AAB91085	Parathyroid hormon
975	13	38.2	35	16	AAR74515	Parathyroid hormon
976	13	38.2	35	16	AAR74516	Parathyroid hormon
977	13	38.2	35	16	AAR74517	Parathyroid hormon
978	13	38.2	35	16	AAR74481	Parathyroid hormon
979	13	38.2	35	16	AAR74482	Parathyroid hormon
980	13	38.2	35	16	AAR74483	Parathyroid hormon
981	13	38.2	35	16	AAR74409	Parathyroid hormon
982	12	35.3	28	23	AAU73105	Parathyroid hormon
983	12	35.3	28	23	AAU73106	Parathyroid hormon
984	12	35.3	28	23	AAU73107	Parathyroid hormon
985	12	35.3	28	23	AAU73108	Parathyroid hormon
986	12	35.3	28	23	AAU73109	Parathyroid hormon
987	12	35.3	29	13	AAR22070	Modified rPTH(7-34
988	12	35.3	31	17	AAR88830	Human parathyroid
989	12	35.3	31	21	AAV96973	Parathyroid hormon
990	12	35.3	31	21	AAV96974	Parathyroid hormon
991	12	35.3	31	21	AAV96975	Parathyroid hormon
992	12	35.3	34	11	AAR08298	Rat parathyroid ho
993	12	35.3	34	14	AAV18002	Human PTH(1-34) de
994	12	35.3	34	19	AAW48396	Human PTH/PTHrP hy
995	12	35.3	34	21	ABJ10759	Human parathyroid
996	12	35.3	34	24	ABP71490	Parathyroid hormon
997	12	35.3	34	24	ABP71491	Parathyroid hormon
998	12	35.3	34	24	ABP71492	Parathyroid hormon
999	12	35.3	34	24	ABP71494	Parathyroid hormon
1000	12	35.3	35	16	AAR74512	Parathyroid hormon

ALIGNMENTS

RESULT 1

AAU73031

ID AAU73031 standard; Peptide; 34 AA.

XX

AC AAU73031;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #13.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;

KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;

KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;

KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;

KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.
 XX
 OS Homo sapiens.
 XX
 PN WO200181415-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Claim 39; Page 26; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 23; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.1e-27;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKLQDVHNF 34
 |||
 Db 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKLQDVHNF 34

RESULT 2

ID AAU73175 standard; Peptide; 35 AA.

AC AAU73175;

DT 12-MAR-2002 (first entry)

DE Parathyroid hormone PTH/PTHrP modulating domain #157.

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;

KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;

KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;

KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;

KW immunoglobulin G; IgG.

OS Synthetic.

PN WO200181415-A2.

PD 01-NOV-2001.

PF 27-APR-2001; 2001WO-US13528.

PR 27-APR-2000; 2000US-200053P.

PR 06-FEB-2001; 2001US-266673P.

XX

XX

XX

XX

PT hormone and parathyroid hormone-related protein receptor modulators -

PS Disclosure; Page 63; 107pp; English.

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and

PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
XX
DR WPI; 1994-018352/03.
XX
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
XX
PS Example 133; Page 40; 92pp; English.
XX
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
XX
SQ Sequence 38 AA;

Query Match 100.0%; Score 34; DB 15; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.3e-27;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKLQDVHNF 34
|||||
Db 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKLQDVHNF 34

RESULT 4

AAU73054

ID AAU73054 standard; Peptide; 30 AA.

XX

AC AAU73054;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #36.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 27; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 30 AA;

Query Match 88.2%; Score 30; DB 23; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2.1e-23;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKLQD 30

RESULT 5

AAAY98046

ID AAY98046 standard; peptide; 28 AA.

XX

AC AAY98046;

XX

DT 04-SEP-2000 (first entry)

XX
 DE Human parathyroid hormone peptide # 6.
 XX
 KW Human; parathyroid hormone; signal transduction; osteoporosis;
 KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;
 KW breast cancer; lung cancer; prostate cancer; multiple myeloma;
 KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;
 KW osteopathic; PTH.
 XX
 OS Homo sapiens.
 XX
 PN WO200031266-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 24-NOV-1999; 99WO-US27863.
 XX
 PR 25-NOV-1998; 98US-0109938.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Bringhurst FR, Takasu H, Gardella TJ, Potts JT;
 XX
 DR WPI; 2000-400076/34.
 XX
 PT Novel biologically active peptide comprising a parathyroid hormone
 PT peptide derivative, useful for treating osteoporosis -
 XX
 PS Claim 9; Page 68; 75pp; English.
 XX
 CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
 CC cells, initiating signal transduction. It has been identified that the
 CC carboxyl terminal of PTH is important for PTH receptor binding, while the
 CC amino terminal is important for signal transduction. Various PTH peptides
 CC were produces with amino- and carboxy terminal modifications which had
 CC varying PTH receptor activation properties and therefore downstream
 CC signalling. Aberrant PTH activity has been implicated in a number of
 CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and
 CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
 CC and a variety of cancers: breast, lung and prostate carcinoma, multiple
 CC myeloma and epidermoid cancers of the head, neck and oesophagus. The
 CC present sequence is a PTH peptide, with a Ser residue at position 1 and
 CC an Arg residue at position 19. The Ser and Arg residues both improve
 CC downstream signalling via phospholipase C (PLC) and ligand binding. The
 CC present peptide may therefore be used as a PTH receptor agonist for the
 CC treatment of the above mentioned disorders. In addition, the present
 CC sequence would be suitable for fracture repair.
 XX
 SQ Sequence 28 AA;

Query Match 82.4%; Score 28; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.2e-21;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKL 28
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKL 28

RESULT 6

AA98042

ID AAY98042 standard; peptide; 28 AA.

XX

AC AAY98042;

XX

DT 04-SEP-2000 (first entry)

XX

DE Human parathyroid hormone peptide # 2.

XX

KW Human; parathyroid hormone; signal transduction; osteoporosis;
KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;
KW breast cancer; lung cancer; prostate cancer; multiple myeloma;
KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;
KW osteopathic; PTH.

XX

OS Homo sapiens.

XX

PN WO200031266-A1.

XX

PD 02-JUN-2000.

XX

PF 24-NOV-1999; 99WO-US27863.

XX

PR 25-NOV-1998; 98US-0109938.

XX

PA (GEHO) GEN HOSPITAL CORP.

XX

PI Bringhurst FR, Takasu H, Gardella TJ, Potts JT;

XX

DR WPI; 2000-400076/34.

XX

PT Novel biologically active peptide comprising a parathyroid hormone
PT peptide derivative, useful for treating osteoporosis -

XX

PS Claim 5; Page 67; 75pp; English.

XX

CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
CC cells, initiating signal transduction. It has been identified that the
CC carboxyl terminal of PTH is important for PTH receptor binding, while the
CC amino terminal is important for signal transduction. Various PTH peptides
CC were produces with amino- and carboxy terminal modifications which had
CC varying PTH receptor activation properties and therefore downstream
CC signalling. Aberrant PTH activity has been implicated in a number of
CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and
CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
CC and a variety of cancers: breast, lung and prostate carcinoma, multiple
CC myeloma and epidermoid cancers of the head, neck and oesophagus. The
CC present sequence is a PTH peptide, with a Gly residue at position 1 and
CC an Arg residue at position 19. The Gly residue reduces downstream
CC signalling via phospholipase C (PLC), whereas the Arg residue restores
CC PLC signalling and ligand binding. The present peptide may therefore be
CC used as a PTH receptor agonist for the treatment of the above mentioned
CC disorders. In addition, the present sequence would be suitable for
CC fracture repair.

XX
SQ Sequence 28 AA;

Query Match 79.4%; Score 27; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMRRVEWLRKKL 28
|||||
Db 2 VSEIQLMHNLGKHLNSMRRVEWLRKKL 28

RESULT 7

AAAY98044

ID AAY98044 standard; peptide; 28 AA.

XX
AC AAY98044;
XX
DT 04-SEP-2000 (first entry)
XX
DE Human parathyroid hormone peptide # 4.
XX
KW Human; parathyroid hormone; signal transduction; osteoporosis;
KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;
KW breast cancer; lung cancer; prostate cancer; multiple myeloma;
KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;
KW osteopathic; PTH.
XX
OS Homo sapiens.
XX
PN WO200031266-A1.
XX
PD 02-JUN-2000.
XX
PF 24-NOV-1999; 99WO-US27863.
XX
PR 25-NOV-1998; 98US-0109938.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Bringhurst FR, Takasu H, Gardella TJ, Potts JT;
XX
DR WPI; 2000-400076/34.
XX
PT Novel biologically active peptide comprising a parathyroid hormone
PT peptide derivative, useful for treating osteoporosis -
XX
PS Claim 6; Page 68; 75pp; English.
XX
CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
CC cells, initiating signal transduction. It has been identified that the
CC carboxyl terminal of PTH is important for PTH receptor binding, while the
CC amino terminal is important for signal transduction. Various PTH peptides
CC were produces with amino- and carboxy terminal modifications which had
CC varying PTH receptor activation properties and therefore downstream
CC signalling. Aberrant PTH activity has been implicated in a number of
CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and

CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
CC and a variety of cancers: breast, lung and prostate carcinoma, multiple
CC myeloma and epidermoid cancers of the head, neck and oesophagus. The
CC present sequence is a PTH peptide, with an Ala residue at position 1 and
CC an Arg residue at position 19. The Ala and Arg residues both improve
CC downstream signalling via phospholipase C (PLC) and ligand binding. The
CC present peptide may therefore be used as a PTH receptor agonist for the
CC treatment of the above mentioned disorders. In addition, the present
CC sequence would be suitable for fracture repair.

XX

SQ Sequence 28 AA;

Query Match 79.4%; Score 27; DB 21; Length 28;

Best Local Similarity 100.0%; Pred. No. 2.2e-20;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMRRVEWLRKKL 28

|||||

Db 2 VSEIQLMHNLGKHLNSMRRVEWLRKKL 28

RESULT 8

AAW08130

ID AAW08130 standard; peptide; 34 AA.

XX

AC AAW08130;

XX

DT 10-OCT-1997 (first entry)

XX

DE Human PTH derivative, [Asp10,Arg19]hPTH(1-34).

XX

KW Human; parathyroid hormone; PTH; cAMP-producing activity;

KW bone formation; osteoporosis; hypoparathyroidism; hypertension;

KW climacteric disturbance.

XX

OS Synthetic.

XX

PN EP748817-A2.

XX

PD 18-DEC-1996.

XX

PF 13-JUN-1996; 96EP-0109475.

XX

PR 15-JUN-1995; 95JP-0148652.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Fukuda T, Habashita J, Nakagawa S, Taketomi S;

XX

DR WPI; 1997-036114/04.

XX

PT New parathyroid hormone derivs. - useful in treatment of bone

PT diseases, hypoparathyroidism and hypertension

XX

PS Example 1; Page 33; 42pp; English.

XX

CC The sequences given in AAW08108-32 represent derivatives of human

CC parathyroid hormone (PTH). These peptides are human PTH (1-34)
CC derivative peptides. They have potent cAMP-producing activity and
CC bone formation activity. They may be used in treatment of bone
CC diseases including osteoporosis, hypoparathyroidism, hypertension
CC and climacteric disturbance. The peptides are low in toxicity and
CC are safe.

XX

SQ Sequence 34 AA;

Query Match 70.6%; Score 24; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LGKHLNSMRRVEWLRKKLQDVHNF 34
|||
Db 11 LGKHLNSMRRVEWLRKKLQDVHNF 34

RESULT 9

AAR22297

ID AAR22297 standard; Peptide; 34 AA.

XX

AC AAR22297;

XX

DT 25-MAR-2003 (updated)

DT 03-AUG-1992 (first entry)

XX

DE Human parathyroid hormone 1-34 [Arg 19, Arg 21].

XX

KW hPTH; protease resistant; osteoporosis; hypoparathyroidism;
KW hypertension.

XX

OS Synthetic.

XX

PN EP477885-A.

XX

PD 01-APR-1992.

XX

PF 25-SEP-1991; 91EP-0116303.

XX

PR 06-SEP-1991; 91JP-0227232.

PR 28-SEP-1990; 90JP-0257490.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Nakagawa S, Fukuda T, Kawase M, Yamazaki I;

XX

DR WPI; 1992-106285/14.

XX

PT New peptide(s) are parathyroid hormone derivs. - used in hormone
PT therapy, for treating osteoporosis hyperparathyroidism and
PT hypertension

XX

PS Claim 9; Page 14; 14pp; English.

XX

CC The peptide is an analogue of human parathyroid hormone fragment
CC 1-34. The peptide modification defined increase resistance to

CC proteases and therefore persistence in the blood. The peptide is
CC used in therapy of osteoporosis, hypoparathyroidism and hypertension.
CC The peptide may be synthesised by the Merrifield solid phase
CC method in an automatic apparatus.
CC See also AAR22290-99.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 34 AA;

Query Match 58.8%; Score 20; DB 13; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMRR 20
|||||||
Db 1 SVSEIQLMHNLGKHLNSMRR 20

RESULT 10

AAB84828

ID AAB84828 standard; Peptide; 34 AA.

XX

AC AAB84828;

XX

DT 25-JUL-2001 (first entry)

XX

DE Parathyroid hormone derivative #19.

XX

KW Osteopathic; calcium homeostasis regulator; parathyroid hormone; PTH;
KW bone mass; osteoporosis.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 34

FT /note= "Optional C-terminal amide"

XX

PN WO200123521-A2.

XX

PD 05-APR-2001.

XX

PF 29-SEP-2000; 2000WO-US26818.

XX

PR 29-SEP-1999; 99US-0156927.

PR 25-FEB-2000; 2000US-0185060.

XX

PA (GEHO) GEN HOSPITAL CORP.

XX

PI Gardella TJ, Kronenberg HM, Potts JT, Juppner H;

XX

DR WPI; 2001-374252/39.

XX

PT New Parathyroid hormone (PTH) derivatives useful for treating
PT conditions characterized by decreases in bone mass -

XX

PS Claim 7; Page 79; 97pp; English.

XX

CC The present invention relates to parathyroid hormone (PTH) polypeptide
CC derivatives, and the present sequence is one such derivative. PTH is a
CC major regulator of calcium homeostasis. The PTH polypeptide derivatives
CC are useful for treating conditions characterised by decreases in bone
CC mass, such as old age osteoporosis and post-menopausal osteoporosis. The
CC polypeptides are also useful for determining rates of bone reformation,
CC bone resorption and/or bone remodeling, by administering the polypeptide
CC to the patient and determining the uptake of the peptide into the bone,
CC and effective bone mass-increasing amount to the peptide is administered
CC by providing to the patient DNA encoding the peptide and expressing the
CC peptide in vivo. The levels of cAMP and inositol phosphate can also be
CC increased in a mammalian cell having PTH-1 receptors, by contacting the
CC cell with a sufficient amount of the polypeptide.

XX

SQ Sequence 34 AA;

Query Match 58.8%; Score 20; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 KHLNSMRRVEWLRKKLQDVH 32
|||
Db 13 KHLNSMRRVEWLRKKLQDVH 32

RESULT 11

AAB96921

ID AAB96921 standard; peptide; 34 AA.

XX

AC AAB96921;

XX

DT 13-JUL-2001 (first entry)

XX

DE Parathyroid hormone derivative #23.

XX

KW Rat; human; parathyroid hormone derivative; calcium homeostasis;

KW hypercalcaemia; anaemia; bone disease; renal impairment; ulcer;

KW myopathy; neuropathy; hyperparathyroidism; osteoporosis; fracture;

KW cartilage disorder.

XX

OS Homo sapiens.

OS Rattus sp.

OS Synthetic.

XX

PN WO200123427-A1.

XX

PD 05-APR-2001.

XX

PF 25-FEB-2000; 2000WO-US04716.

XX

PR 29-SEP-1999; 99US-0156927.

XX

PA (GEHO) GEN HOSPITAL CORP.

XX

PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX

DR WPI; 2001-343161/36.

XX
PT Novel amino acid encoding polypeptides useful in the treatment of
PT osteoporosis -
XX
PS Claim 7; Page 75; 100pp; English.
XX
CC The present invention provides a number of parathyroid hormone
CC derivatives based on the rat and human hormone sequences. These peptides
CC can be used in the treatment of human skeletal conditions, including
CC osteoporosis, fractures and cartilage disorders, disruption of calcium
CC homeostasis, which may cause severe bone disease, anaemia, renal
CC impairment, ulcers, myopathy and neuropathy, hypercalcaemia and
CC hyperparathyroidism. The present peptide was used in the exemplification
CC of the invention.
XX
SQ Sequence 34 AA;

Query Match 58.8%; Score 20; DB 22; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.2e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KHLNSMRRVEWLRKKLQDVH 32
|||||
Db 13 KHLNSMRRVEWLRKKLQDVH 32

RESULT 12

AAR88837

ID AAR88837 standard; peptide; 28 AA.

XX

AC AAR88837;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, hPTH(1-28)-NH2.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; bone loss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 28

FT /note= "amidated"

XX

PN CA2126299-A.

XX

PD 21-DEC-1995.

XX

PF 20-JUN-1994; 94CA-2126299.

XX

PR 20-JUN-1994; 94CA-2126299.

XX

PA (WILL/) WILLICK G E.

XX

PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;

PI Willick GE;
 XX
 DR WPI; 1996-151754/16.
 XX
 PT New human parathyroid hormone analogues - which have increased
 PT adenylyl cyclase activating activity, used for treating osteoporosis
 XX
 PS Claim 1; Fig 10; 21pp; English.
 XX
 CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The
 CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)
 CC activity and reduce protein kinase C (PKC) activity. The analogues
 CC can reverse the loss of bone and increase bone mass and density
 CC without undesirable effects. They are useful for the treatment of
 CC osteoporosis and other bone related disorders and disorders
 CC involving bone cell calcium regulation.
 XX
 SQ Sequence 28 AA;

Query Match 52.9%; Score 18; DB 17; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 13

AAR88838

ID AAR88838 standard; peptide; 28 AA.

XX

AC AAR88838;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, [Leu27]-hPTH(1-28)-NH2.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; bone loss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 28

FT /note= "amidated"

XX

PN CA2126299-A.

XX

PD 21-DEC-1995.

XX

PF 20-JUN-1994; 94CA-2126299.

XX

PR 20-JUN-1994; 94CA-2126299.

XX

PA (WILL/) WILICK G E.

XX
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;
 PI Willick GE;
 XX
 DR WPI; 1996-151754/16.
 XX
 PT New human parathyroid hormone analogues - which have increased
 PT adenylyl cyclase activating activity, used for treating osteoporosis
 XX
 PS Claim 2; Page -; 21pp; English.
 XX
 CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The
 CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)
 CC activity and reduce protein kinase C (PKC) activity. The analogues
 CC can reverse the loss of bone and increase bone mass and density
 CC without undesirable effects. They are useful for the treatment of
 CC osteoporosis and other bone related disorders and disorders
 CC involving bone cell calcium regulation.
 XX
 SQ Sequence 28 AA;

Query Match 52.9%; Score 18; DB 17; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 14

AAY98052

ID AAY98052 standard; peptide; 28 AA.

XX

AC AAY98052;

XX

DT 04-SEP-2000 (first entry)

XX

DE Human parathyroid hormone peptide # 12.

XX

KW Human; parathyroid hormone; signal transduction; osteoporosis;
 KW osteopaenia; hypoparathyroidism; fracture repair; hypercalcaemia;
 KW breast cancer; lung cancer; prostate cancer; multiple myeloma;
 KW hypernephroma; head and neck epidermoid cancer; oesophagus cancer;
 KW osteopathic; PTH.

XX

OS Homo sapiens.

XX

PN WO200031266-A1.

XX

PD 02-JUN-2000.

XX

PF 24-NOV-1999; 99WO-US27863.

XX

PR 25-NOV-1998; 98US-0109938.

XX

PA (GEHO) GEN HOSPITAL CORP.

XX
 PI Bringhurst FR, Takasu H, Gardella TJ, Potts JT;
 XX
 DR WPI; 2000-400076/34.
 XX
 PT Novel biologically active peptide comprising a parathyroid hormone
 PT peptide derivative, useful for treating osteoporosis -
 XX
 PS Disclosure; Page 69; 75pp; English.
 XX
 CC Parathyroid hormone (PTH) binds to PTH receptors in renal and osseous
 CC cells, initiating signal transduction. It has been identified that the
 CC carboxyl terminal of PTH is important for PTH receptor binding, while the
 CC amino terminal is important for signal transduction. Various PTH peptides
 CC were produces with amino- and carboxy terminal modifications which had
 CC varying PTH receptor activation properties and therefore downstream
 CC signalling. Aberrant PTH activity has been implicated in a number of
 CC disorders: osteoporosis, osteopaenia, hypoparathyroidism and
 CC hypercalcaemia. In turn, hypercalcaemia is associated with hypernephroma
 CC and a variety of cancers: breast, lung and prostate carcinoma, multiple
 CC myeloma and epidermoid cancers of the head, neck and oesophagus. The
 CC present sequence is a PTH peptide, with a Ser residue at position 1 and
 CC a Glu residue at position 19. The Ser residue improves downstream
 CC signalling via phospholipase C (PLC), whereas the Glu residue reduces PLC
 CC signalling and ligand binding. PTH peptides with a Arg residue at
 CC position 19 have improved PLC signalling and ligand binding and so may be
 CC used as a PTH receptor agonist for the treatment of the above mentioned
 CC disorders and fracture repair.
 XX
 SQ Sequence 28 AA;

Query Match 52.9%; Score 18; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 15

AAB81074

ID AAB81074 standard; peptide; 28 AA.

XX

AC AAB81074;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human parathyroid hormone analogue SEQ ID 3.

XX

KW Parathyroid hormone; PTH; blood calcium level regulator; osteopathic;
 KW vulnerary; bone growth; bone healing; osteoporosis; fracture; human.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 22
 FT /note= "Forms a beta lactam ring with Lys at position 26"
 FT Modified-site 26
 FT /note= "Forms a beta lactam ring with Glu at position 22"
 FT Modified-site 28
 FT /note= "C-terminal amide"
 XX
 PN WO200121643-A2.
 XX
 PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-CA01083.
 XX
 PR 22-SEP-1999; 99US-0406813.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Barbier J, Morley P, Whitfield J, Willick GE;
 XX
 DR WPI; 2001-308081/32.
 XX
 PT New human parathyroid hormone (hPTH) analog useful for stimulating bone
 PT growth, for restoring bone, for promotion of bone healing, and for
 PT treating osteoporosis and normal fractures -
 XX
 PS Claim 10; Fig 3; 34pp; English.
 XX
 CC Parathyroid hormone (PTH) is a major regulator of blood calcium levels,
 CC this invention relates to hPTH analogues, or their salts. Use of the
 CC analogues results in osteopathic and vulnerary activity. The hPTH
 CC analogues are useful for treating a warm-blooded animal for stimulating
 CC bone growth, for restoring bone, and for the promotion of bone healing
 CC during the treatment of osteoporosis and normal fractures. The present
 CC sequence represents an analogue of human parathyroid hormone.
 XX
 SQ Sequence 28 AA;

Query Match 52.9%; Score 18; DB 22; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 16

AAU73064

ID AAU73064 standard; Peptide; 28 AA.

XX

AC AAU73064;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #46.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;

KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
 KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
 KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.
 XX
 OS Homo sapiens.
 XX
 PN WO200181415-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 27; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 28 AA;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
 |||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 17

AAR11731

ID AAR11731 standard; Protein; 29 AA.

XX

AC AAR11731;

XX

DT 25-MAR-2003 (updated)

DT 03-JUL-1991 (first entry)

XX

DE Adenine-rich PTH-(1-28) in pPTH-AA.

XX

KW Parathyroid hormone; calcium; osteoporosis; bone.

XX

OS Synthetic.

XX

PN W09105050-A.

XX

PD 18-APR-1991.

XX

PF 01-OCT-1990; 90WO-C000335.

XX

PR 29-SEP-1989; 89CA-0615001.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Sung WL;

XX

DR WPI; 1991-132857/18.

DR N-PSDB; AAQ11617.

XX

PT Mature human parathyroid synthesis - includes using eg E. coli

PT transformed by plasmid contg. synthetic nucleotide sequence contg.

PT adenine rich codons in N-terminal region.

XX

PS Disclosure; Fig 3; 62pp; English.

XX

CC The sequence is encoded by adenine rich codons. Codons 29-84

CC (see AAQ11618) are degenerate in the usage frequency favoured by

CC E.coli or yeast. A plasmid contg. the complete sequence expresses

CC PTH with an improved yield. PTH is a blood calcium regulator known

CC to increase bone mass.

CC (Updated on 25-MAR-2003 to correct PR field.)

CC (Updated on 25-MAR-2003 to correct PA field.)

XX

SQ Sequence 29 AA;

Query Match 52.9%; Score 18; DB 12; Length 29;

Best Local Similarity 100.0%; Pred. No. 3e-11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 2 SVSEIQLMHNLGKHLNSM 19

RESULT 18

AAR88836

ID AAR88836 standard; peptide; 29 AA.

XX

AC AAR88836;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, hPTH(1-29)-NH2.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; bone loss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 29

FT /note= "amidated"

XX

PN CA2126299-A.

XX

PD 21-DEC-1995.

XX

PF 20-JUN-1994; 94CA-2126299.

XX

PR 20-JUN-1994; 94CA-2126299.

XX

PA (WILL/) WILLICK G E.

XX

PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;

PI Willick GE;

XX

DR WPI; 1996-151754/16.

XX

PT New human parathyroid hormone analogues - which have increased

PT adenylyl cyclase activating activity, used for treating osteoporosis

XX

PS Claim 1; Fig 9; 21pp; English.

XX

CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The

CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)

CC activity and reduce protein kinase C (PKC) activity. The analogues

CC can reverse the loss of bone and increase bone mass and density

CC without undesirable effects. They are useful for the treatment of

CC osteoporosis and other bone related disorders and disorders

CC involving bone cell calcium regulation.

XX

SQ Sequence 29 AA;

Query Match 52.9%; Score 18; DB 17; Length 29;

Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 19

AAR88839

ID AAR88839 standard; peptide; 29 AA.

XX

AC AAR88839;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, [Leu27]-hPTH(1-29)-NH2.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; bone loss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 29

FT /note= "amidated"

XX

PN CA2126299-A.

XX

PD 21-DEC-1995.

XX

PF 20-JUN-1994; 94CA-2126299.

XX

PR 20-JUN-1994; 94CA-2126299.

XX

PA (WILL/) WILLICK G E.

XX

PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;

PI Willick GE;

XX

DR WPI; 1996-151754/16.

XX

PT New human parathyroid hormone analogues - which have increased

PT adenylyl cyclase activating activity, used for treating osteoporosis

XX

PS Claim 2; Page -; 21pp; English.

XX

CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The

CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)

CC activity and reduce protein kinase C (PKC) activity. The analogues

CC can reverse the loss of bone and increase bone mass and density

CC without undesirable effects. They are useful for the treatment of

CC osteoporosis and other bone related disorders and disorders

CC involving bone cell calcium regulation.

XX

SQ Sequence 29 AA;

Query Match 52.9%; Score 18; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
| | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 20

AAB81075

ID AAB81075 standard; peptide; 29 AA.

XX

AC AAB81075;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human parathyroid hormone analogue SEQ ID 4.

XX

KW Parathyroid hormone; PTH; blood calcium level regulator; osteopathic;
KW vulnerary; bone growth; bone healing; osteoporosis; fracture; human.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 22

FT /note= "Forms a beta lactam ring with Lys at position 26"

FT Modified-site 26

FT /note= "Forms a beta lactam ring with Glu at position 22"

FT Modified-site 29

FT /note= "C-terminal amide"

XX

PN WO200121643-A2.

XX

PD 29-MAR-2001.

XX

PF 21-SEP-2000; 2000WO-CA01083.

XX

PR 22-SEP-1999; 99US-0406813.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Barbier J, Morley P, Whitfield J, Willick GE;

XX

DR WPI; 2001-308081/32.

XX

PT New human parathyroid hormone (HPTH) analog useful for stimulating bone
PT growth, for restoring bone, for promotion of bone healing, and for
PT treating osteoporosis and normal fractures -

XX

PS Claim 11; Fig 4; 34pp; English.

XX

CC Parathyroid hormone (PTH) is a major regulator of blood calcium levels,
CC this invention relates to hPTH analogues, or their salts. Use of the
CC analogues results in osteopathic and vulnerary activity. The hPTH

CC analogues are useful for treating a warm-blooded animal for stimulating
CC bone growth, for restoring bone, and for the promotion of bone healing
CC during the treatment of osteoporosis and normal fractures. The present
CC sequence represents an analogue of human parathyroid hormone.

XX
SQ Sequence 29 AA;

Query Match 52.9%; Score 18; DB 22; Length 29;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSM 18
|||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 21

AAU73063

ID AAU73063 standard; Peptide; 29 AA.

XX

AC AAU73063;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #45.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX
 PS Disclosure; Page 27; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 29 AA;

Query Match 52.9%; Score 18; DB 23; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 22

AAU73179

ID AAU73179 standard; Peptide; 29 AA.

XX

AC AAU73179;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #161.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
 KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
 KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
 KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.

XX

OS Synthetic.

XX

PN WO200181415-A2.
XX
PD 01-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US13528.
XX
PR 27-APR-2000; 2000US-200053P.
PR 28-JUN-2000; 2000US-214860P.
PR 06-FEB-2001; 2001US-266673P.
PR 26-APR-2001; 2001US-0843221.
XX
PA (AMGE-) AMGEN INC.
XX
PI Kostenuik P, Liu C, Lacey DL;
XX
DR WPI; 2002-066435/09.
XX
PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -
XX
PS Disclosure; Page 63; 107pp; English.
XX
CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.
XX
SQ Sequence 29 AA;

Query Match 52.9%; Score 18; DB 23; Length 29;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||
Db 2 SVSEIQLMHNLGKHLNSM 19

RESULT 23
AAR88832
ID AAR88832 standard; peptide; 30 AA.

XX
 AC AAR88832;
 XX
 DT 07-OCT-1996 (first entry)
 XX
 DE Human parathyroid hormone analogue, hPTH(1-30)-NH2.
 XX
 KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;
 KW calcium regulation; reduced PKC activity; protein kinase C;
 KW increased adenylyl cyclase activity; cAMPase; bone loss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 30
 FT /note= "amidated"
 XX
 PN CA2126299-A.
 XX
 PD 21-DEC-1995.
 XX
 PF 20-JUN-1994; 94CA-2126299.
 XX
 PR 20-JUN-1994; 94CA-2126299.
 XX
 PA (WILL/) WILICK G E.
 XX
 PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;
 PI Willick GE;
 XX
 DR WPI; 1996-151754/16.
 XX
 PT New human parathyroid hormone analogues - which have increased
 PT adenylyl cyclase activating activity, used for treating osteoporosis
 XX
 PS Claim 1; Fig 5; 21pp; English.
 XX
 CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The
 CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)
 CC activity and reduce protein kinase C (PKC) activity. The analogues
 CC can reverse the loss of bone and increase bone mass and density
 CC without undesirable effects. They are useful for the treatment of
 CC osteoporosis and other bone related disorders and disorders
 CC involving bone cell calcium regulation.
 XX
 SQ Sequence 30 AA;

Query Match 52.9%; Score 18; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 1 SVSEIQLMHNLGKHLNSM 18

AAR88833

ID AAR88833 standard; peptide; 30 AA.

XX

AC AAR88833;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, [Leu27]-hPTH(1-30)-NH₂.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; bone loss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 30

FT /note= "amidated"

XX

PN CA2126299-A.

XX

PD 21-DEC-1995.

XX

PF 20-JUN-1994; 94CA-2126299.

XX

PR 20-JUN-1994; 94CA-2126299.

XX

PA (WILL/) WILLICK G E.

XX

PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;

PI Willick GE;

XX

DR WPI; 1996-151754/16.

XX

PT New human parathyroid hormone analogues - which have increased

PT adenylyl cyclase activating activity, used for treating osteoporosis

XX

PS Claim 2; Fig 6; 21pp; English.

XX

CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The

CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)

CC activity and reduce protein kinase C (PKC) activity. The analogues

CC can reverse the loss of bone and increase bone mass and density

CC without undesirable effects. They are useful for the treatment of

CC osteoporosis and other bone related disorders and disorders

CC involving bone cell calcium regulation.

XX

SQ Sequence 30 AA;

Query Match 52.9%; Score 18; DB 17; Length 30;

Best Local Similarity 100.0%; Pred. No. 3.1e-11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18

|||||

Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 25

AAW42052

ID AAW42052 standard; peptide; 30 AA.

XX

AC AAW42052;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:7.

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;
KW hypotensive action; bone.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 22

FT /note= "Glu is bound to Lys at position 26 to form
FT a cyclic structure"

FT Modified-site 26

FT /note= "Lys is bound to Glu at position 22 to form
FT a cyclic structure"

FT Modified-site 30

FT /note= "amidated"

XX

PN WO9805683-A1.

XX

PD 12-FEB-1998.

XX

PF 01-AUG-1997; 97WO-CA00547.

XX

PR 14-MAR-1997; 97US-0040560.

PR 02-AUG-1996; 96US-0691647.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;

PI Willick GE;

XX

DR WPI; 1998-145550/13.

XX

PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution
PT - for treating osteoporosis and fractures, also method for screening
PT osteogenic peptide(s) based on their hypotensive action

XX

PS Claim 34; Fig 11; 77pp; English.

XX

CC The present sequence represents a human parathyroid hormone (hPTH)
CC (1-31) peptide analogue. The present invention also describes a method
CC for screening peptides for osteogenic activity by subcutaneous injection
CC of a test compound and seeing if a small drop in arterial pressure
CC occurs after a short time. The hPTH peptide analogue can be useful for
CC stimulating bone growth, restoring bone and promoting bone healing,
CC especially treatment of osteoporosis and normal fractures. The hPTH
CC peptide analogue can be administered by injection or inhalation,

CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
CC the hormone and increases adenylyl cyclase (AC) activity, while
CC cyclisation increases stability against proteases. The screening method,
CC which can be performed in intact female animals, is a quick and simple
CC way of identifying inactive compounds, avoiding the need for long-term,
CC expensive tests on ovariectomised animals.

XX

SQ Sequence 30 AA;

Query Match 52.9%; Score 18; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 26

AAU73051

ID AAU73051 standard; Peptide; 30 AA.

XX

AC AAU73051;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #33.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX
PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -
XX
PS Disclosure; Page 27; 107pp; English.
XX
CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.
XX
SQ Sequence 30 AA;

Query Match 52.9%; Score 18; DB 23; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 27

AAU73062

ID AAU73062 standard; Peptide; 30 AA.

XX

AC AAU73062;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #44.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX
 OS Homo sapiens.
 XX
 PN WO200181415-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 27; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 30 AA;

Query Match 52.9%; Score 18; DB 23; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 28

AAU73136

ID AAU73136 standard; Peptide; 30 AA.

XX

AC AAU73136;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #118.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 31; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's

CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.

XX

SQ Sequence 30 AA;

Query Match 52.9%; Score 18; DB 23; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 29

AAU73137

ID AAU73137 standard; Peptide; 30 AA.

XX

AC AAU73137;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #119.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX
PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -
XX
PS Disclosure; Page 31; 107pp; English.
XX
CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.
XX
SQ Sequence 30 AA;

Query Match 52.9%; Score 18; DB 23; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSM 18
|||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 30

AAU73138

ID AAU73138 standard; Peptide; 30 AA.

XX

AC AAU73138;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #120.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX
 OS Homo sapiens.
 XX
 PN WO200181415-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 31; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 30 AA;

Query Match 52.9%; Score 18; DB 23; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 31

AAU73139

ID AAU73139 standard; Peptide; 30 AA.

XX

AC AAU73139;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #121.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 31; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's

CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.

XX
SQ Sequence 30 AA;

Query Match 52.9%; Score 18; DB 23; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSM 18
|||
DB 1 SVSEIQLMHNLGKHLNSM 18

RESULT 32

AAU73178

ID AAU73178 standard; Peptide; 30 AA.

XX

AC AAU73178;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #160.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Synthetic.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX
PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -
XX
PS Disclosure; Page 63; 107pp; English.
XX
CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.
XX
SQ Sequence 30 AA;

Query Match 52.9%; Score 18; DB 23; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
| | | | | | | | | | | | | | | |
Db 2 SVSEIQLMHNLGKHLNSM 19

RESULT 33
AAW42056
ID AAW42056 standard; peptide; 31 AA.
XX
AC AAW42056;
XX
DT 06-JUL-1998 (first entry)
XX
DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:11.
XX
KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;
KW hypotensive action; bone.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 22
FT /note= "Glu is bound to Lys at position 26 to form

```

FT          a cyclic structure"
FT Modified-site 26
FT          /note= "Lys is bound to Glu at position 22 to form
FT          a cyclic structure"
FT Modified-site 31
FT          /note= "amidated"
XX
PN WO9805683-A1.
XX
PD 12-FEB-1998.
XX
PF 01-AUG-1997; 97WO-CA00547.
XX
PR 14-MAR-1997; 97US-0040560.
PR 02-AUG-1996; 96US-0691647.
XX
PA (CANA ) NAT RES COUNCIL CANADA.
XX
PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;
PI Willick GE;
XX
DR WPI; 1998-145550/13.
XX
PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution
PT - for treating osteoporosis and fractures, also method for screening
PT osteogenic peptide(s) based on their hypotensive action
XX
PS Claim 38; Fig 18; 77pp; English.
XX
CC The present sequence represents a human parathyroid hormone (hPTH)
CC (1-31) peptide analogue. The present invention also describes a method
CC for screening peptides for osteogenic activity by subcutaneous injection
CC of a test compound and seeing if a small drop in arterial pressure
CC occurs after a short time. The hPTH peptide analogue can be useful for
CC stimulating bone growth, restoring bone and promoting bone healing,
CC especially treatment of osteoporosis and normal fractures. The hPTH
CC peptide analogue can be administered by injection or inhalation,
CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
CC the hormone and increases adenylyl cyclase (AC) activity, while
CC cyclisation increases stability against proteases. The screening method,
CC which can be performed in intact female animals, is a quick and simple
CC way of identifying inactive compounds, avoiding the need for long-term,
CC expensive tests on ovariectomised animals.
XX
SQ Sequence 31 AA;

Query Match          52.9%; Score 18; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SVSEIQLMHNLGKHLNSM 18
        |||||
Db      1 SVSEIQLMHNLGKHLNSM 18

```

AAW42057

ID AAW42057 standard; peptide; 31 AA.

XX

AC AAW42057;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:12.

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;

KW hypotensive action; bone.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 22

FT /note= "Glu is bound to Lys at position 26 to form
a cyclic structure"

FT Modified-site 26

FT /note= "Lys is bound to Glu at position 22 to form
a cyclic structure"

FT Modified-site 27

FT /label= Nle

FT /note= "norleucine"

FT Modified-site 31

FT /note= "amidated"

XX

PN WO9805683-A1.

XX

PD 12-FEB-1998.

XX

PF 01-AUG-1997; 97WO-CA00547.

XX

PR 14-MAR-1997; 97US-0040560.

PR 02-AUG-1996; 96US-0691647.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;

PI Willick GE;

XX

DR WPI; 1998-145550/13.

XX

PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution

PT - for treating osteoporosis and fractures, also method for screening

PT osteogenic peptide(s) based on their hypotensive action

XX

PS Claim 39; Fig 19; 77pp; English.

XX

CC The present sequence represents a human parathyroid hormone (hPTH)

CC (1-31) peptide analogue. The present invention also describes a method

CC for screening peptides for osteogenic activity by subcutaneous injection

CC of a test compound and seeing if a small drop in arterial pressure

CC occurs after a short time. The hPTH peptide analogue can be useful for

CC stimulating bone growth, restoring bone and promoting bone healing,

CC especially treatment of osteoporosis and normal fractures. The hPTH

CC peptide analogue can be administered by injection or inhalation,
CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
CC the hormone and increases adenylyl cyclase (AC) activity, while
CC cyclisation increases stability against proteases. The screening method,
CC which can be performed in intact female animals, is a quick and simple
CC way of identifying inactive compounds, avoiding the need for long-term,
CC expensive tests on ovariectomised animals.

XX

SQ Sequence 31 AA;

Query Match 52.9%; Score 18; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 35

AAW42059

ID AAW42059 standard; peptide; 31 AA.

XX

AC AAW42059;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:14.

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;

KW hypotensive action; bone.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 22

FT /note= "Glu is bound to Lys at position 26 to form
FT a cyclic structure"

FT Modified-site 26

FT /note= "Lys is bound to Glu at position 22 to form
FT a cyclic structure"

FT Modified-site 31

FT /note= "amidated"

XX

PN WO9805683-A1.

XX

PD 12-FEB-1998.

XX

PF 01-AUG-1997; 97WO-CA00547.

XX

PR 14-MAR-1997; 97US-0040560.

PR 02-AUG-1996; 96US-0691647.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;
 PI Willick GE;
 XX
 DR WPI; 1998-145550/13.
 XX
 PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution
 PT - for treating osteoporosis and fractures, also method for screening
 PT osteogenic peptide(s) based on their hypotensive action
 XX
 PS Claim 41; Fig 21; 77pp; English.
 XX
 CC The present sequence represents a human parathyroid hormone (hPTH)
 CC (1-31) peptide analogue. The present invention also describes a method
 CC for screening peptides for osteogenic activity by subcutaneous injection
 CC of a test compound and seeing if a small drop in arterial pressure
 CC occurs after a short time. The hPTH peptide analogue can be useful for
 CC stimulating bone growth, restoring bone and promoting bone healing,
 CC especially treatment of osteoporosis and normal fractures. The hPTH
 CC peptide analogue can be administered by injection or inhalation,
 CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
 CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
 CC the hormone and increases adenylyl cyclase (AC) activity, while
 CC cyclisation increases stability against proteases. The screening method,
 CC which can be performed in intact female animals, is a quick and simple
 CC way of identifying inactive compounds, avoiding the need for long-term,
 CC expensive tests on ovariectomised animals.
 XX
 SQ Sequence 31 AA;

 Query Match 52.9%; Score 18; DB 19; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.2e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 36

AAW42060

ID AAW42060 standard; peptide; 31 AA.

XX

AC AAW42060;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:15.

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;
 KW hypotensive action; bone.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 22

FT /note= "Glu is bound to Lys at position 26 to form

FT a cyclic structure"
 FT Modified-site 26
 FT /note= "Lys is bound to Glu at position 22 to form
 FT a cyclic structure"
 FT Modified-site 31
 FT /note= "amidated"
 XX
 PN WO9805683-A1.
 XX
 PD 12-FEB-1998.
 XX
 PF 01-AUG-1997; 97WO-CA00547.
 XX
 PR 14-MAR-1997; 97US-0040560.
 PR 02-AUG-1996; 96US-0691647.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;
 PI Willick GE;
 XX
 DR WPI; 1998-145550/13.
 XX
 PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution
 PT - for treating osteoporosis and fractures, also method for screening
 PT osteogenic peptide(s) based on their hypotensive action
 XX
 PS Claim 42; Fig 22; 77pp; English.
 XX
 CC The present sequence represents a human parathyroid hormone (hPTH)
 CC (1-31) peptide analogue. The present invention also describes a method
 CC for screening peptides for osteogenic activity by subcutaneous injection
 CC of a test compound and seeing if a small drop in arterial pressure
 CC occurs after a short time. The hPTH peptide analogue can be useful for
 CC stimulating bone growth, restoring bone and promoting bone healing,
 CC especially treatment of osteoporosis and normal fractures. The hPTH
 CC peptide analogue can be administered by injection or inhalation,
 CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
 CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
 CC the hormone and increases adenylyl cyclase (AC) activity, while
 CC cyclisation increases stability against proteases. The screening method,
 CC which can be performed in intact female animals, is a quick and simple
 CC way of identifying inactive compounds, avoiding the need for long-term,
 CC expensive tests on ovariectomised animals.
 XX
 SQ Sequence 31 AA;

 Query Match 52.9%; Score 18; DB 19; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.2e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 1 SVSEIQLMHNLGKHLNSM 18

AAW42062

ID AAW42062 standard; peptide; 31 AA.

XX

AC AAW42062;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:17.

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;

KW hypotensive action; bone.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Modified-site	1
FT		/note= "acetylated"
FT	Modified-site	22
FT		/note= "Glu is bound to Lys at position 26 to form
FT		a cyclic structure"
FT	Modified-site	26
FT		/note= "Lys is bound to Glu at position 22 to form
FT		a cyclic structure"
FT	Modified-site	31
FT		/note= "amidated"

XX

PN WO9805683-A1.

XX

PD 12-FEB-1998.

XX

PF 01-AUG-1997; 97WO-CA00547.

XX

PR 14-MAR-1997; 97US-0040560.

PR 02-AUG-1996; 96US-0691647.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;

PI Willick GE;

XX

DR WPI; 1998-145550/13.

XX

PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution

PT - for treating osteoporosis and fractures, also method for screening

PT osteogenic peptide(s) based on their hypotensive action

XX

PS Claim 44; Fig 24; 77pp; English.

XX

CC The present sequence represents a human parathyroid hormone (hPTH)

CC (1-31) peptide analogue. The present invention also describes a method

CC for screening peptides for osteogenic activity by subcutaneous injection

CC of a test compound and seeing if a small drop in arterial pressure

CC occurs after a short time. The hPTH peptide analogue can be useful for

CC stimulating bone growth, restoring bone and promoting bone healing,

CC especially treatment of osteoporosis and normal fractures. The hPTH

CC peptide analogue can be administered by injection or inhalation,

CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
CC the hormone and increases adenylyl cyclase (AC) activity, while
CC cyclisation increases stability against proteases. The screening method,
CC which can be performed in intact female animals, is a quick and simple
CC way of identifying inactive compounds, avoiding the need for long-term,
CC expensive tests on ovariectomised animals.

XX
SQ Sequence 31 AA;

Query Match 52.9%; Score 18; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSM 18
|||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 38

AAW42063

ID AAW42063 standard; peptide; 31 AA.

XX
AC AAW42063;

XX
DT 06-JUL-1998 (first entry)

XX
DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:18.

XX
KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;
KW hypotensive action; bone.

XX
OS Synthetic.
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Modified-site 22
FT /note= "Lys is bound to Glu at position 26 to form
FT a cyclic structure"
FT Modified-site 26
FT /note= "Glu is bound to Lys at position 22 to form
FT a cyclic structure"
FT Modified-site 31
FT /note= "amidated"

XX
PN WO9805683-A1.

XX
PD 12-FEB-1998.

XX
PF 01-AUG-1997; 97WO-CA00547.

XX
PR 14-MAR-1997; 97US-0040560.

XX
PR 02-AUG-1996; 96US-0691647.

XX
PA (CANA) NAT RES COUNCIL CANADA.

XX
PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;

PI Willick GE;
 XX
 DR WPI; 1998-145550/13.
 XX
 PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution
 PT - for treating osteoporosis and fractures, also method for screening
 PT osteogenic peptide(s) based on their hypotensive action
 XX
 PS Claim 45; Fig 25; 77pp; English.
 XX
 CC The present sequence represents a human parathyroid hormone (hPTH)
 CC (1-31) peptide analogue. The present invention also describes a method
 CC for screening peptides for osteogenic activity by subcutaneous injection
 CC of a test compound and seeing if a small drop in arterial pressure
 CC occurs after a short time. The hPTH peptide analogue can be useful for
 CC stimulating bone growth, restoring bone and promoting bone healing,
 CC especially treatment of osteoporosis and normal fractures. The hPTH
 CC peptide analogue can be administered by injection or inhalation,
 CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
 CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
 CC the hormone and increases adenylyl cyclase (AC) activity; while
 CC cyclisation increases stability against proteases. The screening method,
 CC which can be performed in intact female animals, is a quick and simple
 CC way of identifying inactive compounds, avoiding the need for long-term,
 CC expensive tests on ovariectomised animals.
 XX
 SQ Sequence 31 AA;

 Query Match 52.9%; Score 18; DB 19; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.2e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 39

AAW42065

ID AAW42065 standard; peptide; 31 AA.

XX

AC AAW42065;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:20.

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;
 KW hypotensive action; bone.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 22..26

FT Modified-site 31

FT /note= "amidated"

XX
 PN WO9805683-A1.
 XX
 PD 12-FEB-1998.
 XX
 PF 01-AUG-1997; 97WO-CA00547.
 XX
 PR 14-MAR-1997; 97US-0040560.
 PR 02-AUG-1996; 96US-0691647.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;
 PI Willick GE;
 XX
 DR WPI; 1998-145550/13.
 XX
 PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution
 PT - for treating osteoporosis and fractures, also method for screening
 PT osteogenic peptide(s) based on their hypotensive action
 XX
 PS Disclosure; Fig 27; 77pp; English.
 XX
 CC The present sequence represents a human parathyroid hormone (hPTH)
 CC (1-31) peptide analogue. The present invention also describes a method
 CC for screening peptides for osteogenic activity by subcutaneous injection
 CC of a test compound and seeing if a small drop in arterial pressure
 CC occurs after a short time. The hPTH peptide analogue can be useful for
 CC stimulating bone growth, restoring bone and promoting bone healing,
 CC especially treatment of osteoporosis and normal fractures. The hPTH
 CC peptide analogue can be administered by injection or inhalation,
 CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
 CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
 CC the hormone and increases adenylyl cyclase (AC) activity, while
 CC cyclisation increases stability against proteases. The screening method,
 CC which can be performed in intact female animals, is a quick and simple
 CC way of identifying inactive compounds, avoiding the need for long-term,
 CC expensive tests on ovariectomised animals.
 XX
 SQ Sequence 31 AA;

 Query Match 52.9%; Score 18; DB 19; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.2e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 1 SVSEIQLMHNLGKHLNSM 18

 RESULT 40
 AAW42066
 ID AAW42066 standard; peptide; 31 AA.
 XX
 AC AAW42066;
 XX
 DT 06-JUL-1998 (first entry)

XX
 DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:21.
 XX
 KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;
 KW hypotensive action; bone.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 26..30
 FT Modified-site 31
 FT /note= "amidated"
 XX
 PN WO9805683-A1.
 XX
 PD 12-FEB-1998.
 XX
 PF 01-AUG-1997; 97WO-CA00547.
 XX
 PR 14-MAR-1997; 97US-0040560.
 PR 02-AUG-1996; 96US-0691647.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;
 PI Willick GE;
 XX
 DR WPI; 1998-145550/13.
 XX
 PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution
 PT - for treating osteoporosis and fractures, also method for screening
 PT osteogenic peptide(s) based on their hypotensive action
 XX
 PS Disclosure; Fig 28; 77pp; English.
 XX
 CC The present sequence represents a human parathyroid hormone (hPTH)
 CC (1-31) peptide analogue. The present invention also describes a method
 CC for screening peptides for osteogenic activity by subcutaneous injection
 CC of a test compound and seeing if a small drop in arterial pressure
 CC occurs after a short time. The hPTH peptide analogue can be useful for
 CC stimulating bone growth, restoring bone and promoting bone healing,
 CC especially treatment of osteoporosis and normal fractures. The hPTH
 CC peptide analogue can be administered by injection or inhalation,
 CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
 CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
 CC the hormone and increases adenylyl cyclase (AC) activity, while
 CC cyclisation increases stability against proteases. The screening method,
 CC which can be performed in intact female animals, is a quick and simple
 CC way of identifying inactive compounds, avoiding the need for long-term,
 CC expensive tests on ovariectomised animals.
 XX
 SQ Sequence 31 AA;

 Query Match 52.9%; Score 18; DB 19; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.2e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
| | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSM 18

Search completed: January 14, 2004, 10:34:22
Job time : 33.5171 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 10.0623 Seconds
 (without alignments)
 324.949 Million cell updates/sec

Title: US-09-843-221A-164
 Perfect score: 34
 Sequence: 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKLQDVHNF 34

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3709

Minimum DB seq length: 28
 Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : PIR_76:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	14.7	34	2	A84241	hypothetical prote
2	5	14.7	34	2	B97032	transcription regu
3	5	14.7	35	2	E95098	hypothetical prote
4	4	11.8	28	2	T09594	gene LFY protein -
5	4	11.8	29	1	A55527	pyrroloquinoline q
6	4	11.8	29	2	S01614	dystrophin - rat (
7	4	11.8	29	2	I78537	copper transportin
8	4	11.8	29	2	S78412	ribosomal protein
9	4	11.8	30	2	S01657	atrial natriuretic
10	4	11.8	30	2	S21195	spectrin beta chai
11	4	11.8	30	2	S63531	hypothetical prote
12	4	11.8	31	2	S44471	glucagon G1 - Nort
13	4	11.8	31	2	S44472	glucagon G2 - Nort

14	4	11.8	31	2	D70236	hypothetical prote
15	4	11.8	32	2	F23454	ovalbumin phosphos
16	4	11.8	32	2	G84161	hypothetical prote
17	4	11.8	32	2	S22304	hypothetical prote
18	4	11.8	33	2	E81714	hypothetical prote
19	4	11.8	34	2	B97232	hypothetical prote
20	4	11.8	35	2	D23454	ovalbumin phosphos
21	4	11.8	35	2	G23454	ovalbumin phosphos
22	4	11.8	35	2	B24677	Balbani ring 2 ch
23	4	11.8	35	2	D82125	hypothetical prote
24	4	11.8	36	2	F95057	hypothetical prote
25	4	11.8	36	2	A84774	hypothetical prote
26	4	11.8	37	2	D47099	hypothetical prote
27	4	11.8	37	2	T12635	homeotic protein H
28	4	11.8	39	1	CKFHCS	sarcotoxin IC - fl
29	4	11.8	39	2	S77164	ycf32 protein - Sy
30	4	11.8	40	2	S52343	hypothetical prote
31	3	8.8	28	1	LFECCL	leu operon leader
32	3	8.8	28	2	A42272	brain-type creatin
33	3	8.8	28	2	C32416	phospholipase A2 (
34	3	8.8	28	2	B60071	vasoactive intesti
35	3	8.8	28	2	A60304	vasoactive intesti
36	3	8.8	28	2	PN0047	signal transductio
37	3	8.8	28	2	G90638	leu operon leader
38	3	8.8	28	2	S56121	type I DNA methylt
39	3	8.8	28	2	S70894	hypothetical prote
40	3	8.8	28	2	S22469	hypothetical prote
41	3	8.8	28	2	S26254	rel protein - chic
42	3	8.8	28	2	I59477	antigen, T-cell re
43	3	8.8	28	2	F46522	T-cell receptor et
44	3	8.8	28	2	G85489	leu operon leader
45	3	8.8	28	2	H85908	hypothetical prote
46	3	8.8	29	1	GCCB	glucagon - Chinch
47	3	8.8	29	2	A61509	islet amyloid poly
48	3	8.8	29	2	S17147	galanin - chicken
49	3	8.8	29	2	I52628	low affinity nerve
50	3	8.8	29	2	A05272	gelsolin, cytosoli
51	3	8.8	29	2	B44101	calmodulin, vasoac
52	3	8.8	29	2	S42642	probable rhicadhes
53	3	8.8	29	2	A00774	3-oxoadipate enol-
54	3	8.8	29	2	B81136	hypothetical prote
55	3	8.8	29	2	I84189	cyclic AMP recepto
56	3	8.8	29	2	S65747	CDP-paratose synth
57	3	8.8	29	2	S65748	CDP-paratose synth
58	3	8.8	29	2	B41476	probable antigen 2
59	3	8.8	29	2	S68094	2,3-dihydroxybenzo
60	3	8.8	29	2	A27688	mammary-derived gr
61	3	8.8	29	2	T31443	cytochrome bc chai
62	3	8.8	29	2	F85570	hypothetical prote
63	3	8.8	29	2	I49732	NADH2 dehydrogenas
64	3	8.8	29	2	A59479	NADP phosphatase I
65	3	8.8	30	1	IRTRC2	protamine 1a - rai
66	3	8.8	30	1	CLHRY2	protamine YII - Pa
67	3	8.8	30	1	CLHR2A	protamine YII - At
68	3	8.8	30	2	S40309	tyrosine 3-monooxy
69	3	8.8	30	2	C21897	ornithine carbamoy
70	3	8.8	30	2	A28562	glutathione transf

71	3	8.8	30	2	A05315	pancreatic ribonuc
72	3	8.8	30	2	A44598	endo-1,4-beta-xyla
73	3	8.8	30	2	A61333	trypsin (EC 3.4.21
74	3	8.8	30	2	A44912	cysteine proteinas
75	3	8.8	30	2	B61125	glucagon-like pept
76	3	8.8	30	2	C61125	glucagon-like pept
77	3	8.8	30	2	C59076	defensin alpha-3 -
78	3	8.8	30	2	PD0013	cAMP response elem
79	3	8.8	30	2	S11617	ribosomal protein
80	3	8.8	30	2	S07217	ribosomal protein
81	3	8.8	30	2	PC4172	profilin - rat (fr
82	3	8.8	30	2	A34461	heat shock protein
83	3	8.8	30	2	A22977	delta-endotoxin -
84	3	8.8	30	2	A44913	34K core flagella
85	3	8.8	30	2	S08565	ribulose-bisphosph
86	3	8.8	30	2	PQ0444	hypothetical prote
87	3	8.8	30	2	B95020	hypothetical prote
88	3	8.8	30	2	H95021	hypothetical prote
89	3	8.8	30	2	D72276	hypothetical prote
90	3	8.8	30	2	D70253	conserved hypothet
91	3	8.8	30	2	B81956	hypothetical prote
92	3	8.8	30	2	E82294	hypothetical prote
93	3	8.8	30	2	D82251	hypothetical prote
94	3	8.8	30	2	A35687	probable 39K inorg
95	3	8.8	30	2	S73316	photosystem I chai
96	3	8.8	30	2	A32946	trypsin-like serin
97	3	8.8	30	2	PL0189	Ig light chain - s
98	3	8.8	30	2	S65519	carcinoembryonic a
99	3	8.8	30	2	S34765	4-hydroxybutyryl-C
100	3	8.8	30	2	D81532	hypothetical prote
101	3	8.8	30	2	A48923	retrovirus-related
102	3	8.8	30	2	B56586	storage hexamer 2
103	3	8.8	30	2	F81360	very hypothetical
104	3	8.8	30	2	S15650	NADH2 dehydrogenas
105	3	8.8	30	4	I52605	hypothetical MLL/E
106	3	8.8	31	1	A28805	leiurotoxin I [val
107	3	8.8	31	1	A49078	leiurotoxin I-like
108	3	8.8	31	1	CLHRZ	protamine Z - Paci
109	3	8.8	31	1	CLHRZA	protamine Z - Atla
110	3	8.8	31	1	S34504	photosystem I prot
111	3	8.8	31	2	T44925	hypothetical prote
112	3	8.8	31	2	S39019	glucagon-like pept
113	3	8.8	31	2	A58793	relaxin chain B -
114	3	8.8	31	2	A58586	conotoxin MrVIA -
115	3	8.8	31	2	F30608	Ig kappa chain V-I
116	3	8.8	31	2	D30608	Ig kappa chain V-I
117	3	8.8	31	2	S03295	Ig alpha chain C r
118	3	8.8	31	2	S03297	Ig alpha chain C r
119	3	8.8	31	2	I51349	protamine - rainbo
120	3	8.8	31	2	I52232	tau protein - huma
121	3	8.8	31	2	A36162	neutrophil-activat
122	3	8.8	31	2	PW0047	estrogen receptor
123	3	8.8	31	2	S04980	ferritin heavy cha
124	3	8.8	31	2	S32610	antiviral protein
125	3	8.8	31	2	S38881	inner membrane pro
126	3	8.8	31	2	G95018	hypothetical prote
127	3	8.8	31	2	A95085	hypothetical prote

128	3	8.8	31	2	H95093	hypothetical prote
129	3	8.8	31	2	E95140	hypothetical prote
130	3	8.8	31	2	E95151	hypothetical prote
131	3	8.8	31	2	H72808	gp82.2 protein - M
132	3	8.8	31	2	E70202	hypothetical prote
133	3	8.8	31	2	E70223	hypothetical prote
134	3	8.8	31	2	H70225	hypothetical prote
135	3	8.8	31	2	C70240	hypothetical prote
136	3	8.8	31	2	H70252	hypothetical prote
137	3	8.8	31	2	E64562	hypothetical prote
138	3	8.8	31	2	C71845	hypothetical prote
139	3	8.8	31	2	S49191	hypothetical prote
140	3	8.8	31	2	B81027	lacto-N-neotetraos
141	3	8.8	31	2	H82353	hypothetical prote
142	3	8.8	31	2	A05051	hypothetical prote
143	3	8.8	31	2	B23605	histone H1.3 - whe
144	3	8.8	31	2	S78738	protein YOL038c-a
145	3	8.8	31	2	A36221	cecropin P1 - pig
146	3	8.8	31	2	C84082	hypothetical prote
147	3	8.8	31	2	D81591	hypothetical prote
148	3	8.8	31	2	G81558	hypothetical prote
149	3	8.8	31	2	G82816	hypothetical prote
150	3	8.8	31	2	F82565	hypothetical prote
151	3	8.8	32	1	TCEE	calcitonin - Japan
152	3	8.8	32	1	TCON2	calcitonin 2 - soc
153	3	8.8	32	1	TCON2C	calcitonin 2 - chu
154	3	8.8	32	1	TCON2P	calcitonin 2 - pin
155	3	8.8	32	1	TCON3	calcitonin 3 - coh
156	3	8.8	32	1	IRTR2	protamine II - rai
157	3	8.8	32	2	S20719	alcohol dehydrogen
158	3	8.8	32	2	A61143	trypsin (EC 3.4.21
159	3	8.8	32	2	B40186	ubiquitin / riboso
160	3	8.8	32	2	S57780	histone H3 - rice
161	3	8.8	32	2	I51089	protamine - Japane
162	3	8.8	32	2	A24047	gap junction prote
163	3	8.8	32	2	S51524	anchorin CII - bov
164	3	8.8	32	2	S36809	GTP-binding regula
165	3	8.8	32	2	A29743	translation initia
166	3	8.8	32	2	A03367	lectin - Macrotylo
167	3	8.8	32	2	A44900	fimbrin, SEF 21 -
168	3	8.8	32	2	S03273	photosystem II oxy
169	3	8.8	32	2	C46107	polyomavirus enhan
170	3	8.8	32	2	S08482	regulatory protein
171	3	8.8	32	2	A95108	hypothetical prote
172	3	8.8	32	2	E87694	hypothetical prote
173	3	8.8	32	2	E70225	hypothetical prote
174	3	8.8	32	2	B70241	hypothetical prote
175	3	8.8	32	2	B70257	hypothetical prote
176	3	8.8	32	2	D82353	hypothetical prote
177	3	8.8	32	2	E82279	hypothetical prote
178	3	8.8	32	2	E82089	hypothetical prote
179	3	8.8	32	2	H82416	hypothetical prote
180	3	8.8	32	2	T17394	vrlN protein - Dic
181	3	8.8	32	2	S23476	hypothetical prote
182	3	8.8	32	2	S78323	photosystem II pro
183	3	8.8	32	2	A05015	hypothetical prote
184	3	8.8	32	2	T14569	hypothetical prote

185	3	8.8	32	2	H84081	hypothetical prote
186	3	8.8	32	2	F82833	hypothetical prote
187	3	8.8	32	2	JC5802	ovulation stimulat
188	3	8.8	32	2	E85588	hypothetical prote
189	3	8.8	33	1	IRTR1B	protamine IB - rai
190	3	8.8	33	1	IRTR1A	protamine IA - rai
191	3	8.8	33	2	S43312	2',3'-cyclic-nucle
192	3	8.8	33	2	S26859	chitinase (EC 3.2.
193	3	8.8	33	2	I52219	c-ras-Ki-2 protein
194	3	8.8	33	2	I53221	K-ras protein - hu
195	3	8.8	33	2	PC2300	gaegurin 1 - Korea
196	3	8.8	33	2	I56451	relaxin - hamadrya
197	3	8.8	33	2	PC2205	interferon-alpha L
198	3	8.8	33	2	A31461	T-cell receptor de
199	3	8.8	33	2	A26762	protamine (mugilin
200	3	8.8	33	2	B26762	protamine (mugilin
201	3	8.8	33	2	I49415	gamma4-crystallin
202	3	8.8	33	2	A03150	retinoic acid-bind
203	3	8.8	33	2	C46027	neurotransmitter t
204	3	8.8	33	2	PQ0150	dnaK-type molecula
205	3	8.8	33	2	B44906	L1 protein - human
206	3	8.8	33	2	PQ0418	matrix protein M1
207	3	8.8	33	2	S34505	hypothetical prote
208	3	8.8	33	2	G95006	hypothetical prote
209	3	8.8	33	2	C95200	hypothetical prote
210	3	8.8	33	2	A87213	hypothetical prote
211	3	8.8	33	2	F84163	hypothetical prote
212	3	8.8	33	2	E82135	hypothetical prote
213	3	8.8	33	2	H82475	hypothetical prote
214	3	8.8	33	2	A41822	antimicrobial pept
215	3	8.8	33	2	S68096	lactate dehydrogen
216	3	8.8	33	2	E82526	hypothetical prote
217	3	8.8	33	2	G85600	hypothetical prote
218	3	8.8	33	2	H85651	hypothetical prote
219	3	8.8	33	2	AC1012	hypothetical prote
220	3	8.8	33	2	C97406	hypothetical prote
221	3	8.8	34	1	TYTUY2	protamine Y2 - blu
222	3	8.8	34	1	TYTUZ1	protamine Z1 - blu
223	3	8.8	34	1	TYTUZ2	protamine Z2 - blu
224	3	8.8	34	2	S57282	phospholipase A2 (
225	3	8.8	34	2	A40298	dermaseptin - Sauv
226	3	8.8	34	2	JS0426	big gastrin - goat
227	3	8.8	34	2	JN0582	protamine (scombri
228	3	8.8	34	2	JX0203	protamine Z1 - str
229	3	8.8	34	2	JX0204	protamine Z2 - str
230	3	8.8	34	2	I49410	gamma-crystallin-1
231	3	8.8	34	2	D48147	troponin I (altern
232	3	8.8	34	2	A43564	neurogenic protein
233	3	8.8	34	2	B26021	traY protein - Esc
234	3	8.8	34	2	H95047	hypothetical prote
235	3	8.8	34	2	D95189	hypothetical prote
236	3	8.8	34	2	F70242	hypothetical prote
237	3	8.8	34	2	B70252	hypothetical prote
238	3	8.8	34	2	F81919	hypothetical prote
239	3	8.8	34	2	H81883	hypothetical prote
240	3	8.8	34	2	F81044	hypothetical prote
241	3	8.8	34	2	F82163	hypothetical prote

242	3	8.8	34	2	E82100	hypothetical prote
243	3	8.8	34	2	B82449	hypothetical prote
244	3	8.8	34	2	S13662	cellulase (EC 3.2.
245	3	8.8	34	2	A60110	repetitive protein
246	3	8.8	34	2	S44828	F54F2.3 protein -
247	3	8.8	34	2	S77985	cytochrome-c oxida
248	3	8.8	34	2	S40662	P-cadherin - mouse
249	3	8.8	34	2	F84079	hypothetical prote
250	3	8.8	34	2	H81600	hypothetical prote
251	3	8.8	34	2	C82819	hypothetical prote
252	3	8.8	34	2	C82764	hypothetical prote
253	3	8.8	34	2	S12554	hydroxymethylgluta
254	3	8.8	35	2	S71915	hemoglobin, extrac
255	3	8.8	35	2	A05302	hemoglobin beta ch
256	3	8.8	35	2	A29663	histone H4 - starf
257	3	8.8	35	2	S27154	ribosomal protein
258	3	8.8	35	2	E48401	ribosomal protein
259	3	8.8	35	2	S13435	lectin III - furze
260	3	8.8	35	2	S74556	photosystem II psb
261	3	8.8	35	2	S18224	filamentous hemagg
262	3	8.8	35	2	S18226	opacity protein op
263	3	8.8	35	2	T07870	major latex protei
264	3	8.8	35	2	B33770	hypothetical prote
265	3	8.8	35	2	I48925	homeobox protein -
266	3	8.8	35	2	C96619	protein T30E16.7 [
267	3	8.8	35	2	B84674	hypothetical prote
268	3	8.8	35	2	F84395	hypothetical prote
269	3	8.8	35	2	B82012	hypothetical prote
270	3	8.8	35	2	A82151	hypothetical prote
271	3	8.8	35	2	F82051	hypothetical prote
272	3	8.8	35	2	I64003	hypothetical prote
273	3	8.8	35	2	S58708	neutral phosphatas
274	3	8.8	35	2	F69827	hypothetical prote
275	3	8.8	35	2	C69977	hypothetical prote
276	3	8.8	35	2	T06314	alpha-amylase homo
277	3	8.8	35	2	G60529	hemocyanin M3' - c
278	3	8.8	35	2	A38107	mammalian toxin -
279	3	8.8	35	2	S49309	oncofetal protein
280	3	8.8	35	2	C81560	hypothetical prote
281	3	8.8	35	2	B85708	unknown protein en
282	3	8.8	35	2	AI0076	hypothetical prote
283	3	8.8	36	2	B60413	pancreatic hormone
284	3	8.8	36	2	S08552	ribosomal protein
285	3	8.8	36	2	S72299	ribosomal protein
286	3	8.8	36	2	B44400	myosin heavy chain
287	3	8.8	36	2	B31872	retinoic acid-bind
288	3	8.8	36	2	S35572	zona pellucida pro
289	3	8.8	36	2	B41481	virulence-associat
290	3	8.8	36	2	A38659	methanol dehydroge
291	3	8.8	36	2	C95218	conserved domain p
292	3	8.8	36	2	E84416	hypothetical prote
293	3	8.8	36	2	S17834	acetyl-CoA carboxy
294	3	8.8	36	2	E70220	hypothetical prote
295	3	8.8	36	2	E70238	hypothetical prote
296	3	8.8	36	2	F64604	hypothetical prote
297	3	8.8	36	2	G81853	hypothetical prote
298	3	8.8	36	2	S16552	hypothetical prote

299	3	8.8	36	2	A82163	hypothetical prote
300	3	8.8	36	2	C82111	hypothetical prote
301	3	8.8	36	2	A82092	hypothetical prote
302	3	8.8	36	2	B82093	hypothetical prote
303	3	8.8	36	2	A82437	hypothetical prote
304	3	8.8	36	2	A38729	pyruvate decarboxy
305	3	8.8	36	2	S46227	hypothetical prote
306	3	8.8	36	2	S67795	probable membrane
307	3	8.8	36	2	T22263	hypothetical prote
308	3	8.8	36	2	A57443	guanylate cyclase
309	3	8.8	36	2	D83682	hypothetical prote
310	3	8.8	36	2	A83870	hypothetical prote
311	3	8.8	36	2	F84074	hypothetical prote
312	3	8.8	36	2	A56634	neuropeptide F - A
313	3	8.8	36	2	S77071	probable plastoqui
314	3	8.8	36	2	AF1015	hypothetical prote
315	3	8.8	36	2	AI1841	hypothetical prote
316	3	8.8	37	1	S32792	iberiotoxin - east
317	3	8.8	37	1	HSWT93	histone H2A.3 - wh
318	3	8.8	37	2	S48656	fusicoccin recepto
319	3	8.8	37	2	S03570	trypsin (EC 3.4.21
320	3	8.8	37	2	S39367	proteinase omega -
321	3	8.8	37	2	S06217	transforming prote
322	3	8.8	37	2	S05037	insulinoma amyloid
323	3	8.8	37	2	A30607	Ig kappa chain V-I
324	3	8.8	37	2	S71912	hemoglobin, extrac
325	3	8.8	37	2	D87154	50S ribosomal prot
326	3	8.8	37	2	PC1121	antifungal 25K pro
327	3	8.8	37	2	G01887	MEK kinase - human
328	3	8.8	37	2	S07517	gene 6.3 protein -
329	3	8.8	37	2	G70223	hypothetical prote
330	3	8.8	37	2	E70241	hypothetical prote
331	3	8.8	37	2	D83199	hypothetical prote
332	3	8.8	37	2	H82304	hypothetical prote
333	3	8.8	37	2	S21132	photosystem II cyt
334	3	8.8	37	2	F59103	hypothetical prote
335	3	8.8	37	2	T36662	small hypothetical
336	3	8.8	37	2	T11815	hypothetical prote
337	3	8.8	37	2	A57127	diuretic hormone 1
338	3	8.8	37	2	I50036	MHC class I protei
339	3	8.8	37	2	C32112	R15 gamma peptide
340	3	8.8	37	2	B48845	sterol regulatory
341	3	8.8	37	2	S68261	hypothetical prote
342	3	8.8	37	2	S49982	Tcell receptor alp
343	3	8.8	37	2	B39030	androgen-binding p
344	3	8.8	37	2	PN0550	metabotropic gluta
345	3	8.8	37	2	G95919	probable transposa
346	3	8.8	37	2	S70931	histone-like prote
347	3	8.8	37	2	F81403	hypothetical prote
348	3	8.8	37	2	AH0637	conserved hypothet
349	3	8.8	38	1	R5EC36	ribosomal protein
350	3	8.8	38	1	G8BPSV	gene 8 protein - s
351	3	8.8	38	2	C34047	stylar glycoprotei
352	3	8.8	38	2	T11763	acetyl-CoA carboxy
353	3	8.8	38	2	S39034	lipid transfer pro
354	3	8.8	38	2	A42974	natriuretic peptid
355	3	8.8	38	2	A49165	pituitary adenylat

356	3	8.8	38	2	A61070	pituitary adenylat
357	3	8.8	38	2	PS0129	H-2 class I histoc
358	3	8.8	38	2	S50764	ribosomal protein
359	3	8.8	38	2	E72247	ribosomal protein
360	3	8.8	38	2	H83113	50S ribosomal prot
361	3	8.8	38	2	AG0028	50S ribosomal prot
362	3	8.8	38	2	D91149	50S ribosomal subu
363	3	8.8	38	2	AF1008	50S ribosomal chai
364	3	8.8	38	2	PH1920	annexin-like 40K p
365	3	8.8	38	2	S72344	pile protein - Nei
366	3	8.8	38	2	A60216	hyperglycemic horm
367	3	8.8	38	2	T06971	hypothetical prote
368	3	8.8	38	2	S65416	pyruvate synthase
369	3	8.8	38	2	B95069	hypothetical prote
370	3	8.8	38	2	A95139	hypothetical prote
371	3	8.8	38	2	H91111	hypothetical prote
372	3	8.8	38	2	D90631	hypothetical prote
373	3	8.8	38	2	E72306	hypothetical prote
374	3	8.8	38	2	E81873	hypothetical prote
375	3	8.8	38	2	T14885	hypothetical prote
376	3	8.8	38	2	A82478	hypothetical prote
377	3	8.8	38	2	E82463	hypothetical prote
378	3	8.8	38	2	A82450	hypothetical prote
379	3	8.8	38	2	D37842	hypothetical prote
380	3	8.8	38	2	G75398	conserved hypothet
381	3	8.8	38	2	B69492	hypothetical prote
382	3	8.8	38	2	S23173	photosystem I chai
383	3	8.8	38	2	T01992	hypothetical prote
384	3	8.8	38	2	S58601	hypothetical prote
385	3	8.8	38	2	T01741	hypothetical prote
386	3	8.8	38	2	B39888	synapsin I - bovin
387	3	8.8	38	2	S02600	hypothetical prote
388	3	8.8	38	2	B49012	orf 5' of megl - m
389	3	8.8	38	2	A83863	hypothetical prote
390	3	8.8	38	2	H81603	hypothetical prote
391	3	8.8	38	2	E71260	hypothetical prote
392	3	8.8	38	2	E82858	hypothetical prote
393	3	8.8	38	2	G71305	probable ribosomal
394	3	8.8	38	2	B97327	hypothetical prote
395	3	8.8	38	2	E86077	hypothetical prote
396	3	8.8	38	2	H85994	50S ribosomal subu
397	3	8.8	38	2	T08652	hypothetical prote
398	3	8.8	38	2	AB0747	hypothetical prote
399	3	8.8	38	2	AH0774	hypothetical prote
400	3	8.8	38	2	C97551	hypothetical prote
401	3	8.8	39	1	HWGH3Z	exendin-3 - Mexica
402	3	8.8	39	1	HWGH4G	exendin-4 - Gila m
403	3	8.8	39	2	B45946	gamma-glutamyltran
404	3	8.8	39	2	I55325	aspartate transami
405	3	8.8	39	2	S09645	hygromycin-B kinas
406	3	8.8	39	2	C55995	prostaglandin E2 r
407	3	8.8	39	2	S07458	Ig kappa chain V r
408	3	8.8	39	2	PH0878	Ig kappa chain V r
409	3	8.8	39	2	S71913	hemoglobin, extrac
410	3	8.8	39	2	S72459	ribosomal protein
411	3	8.8	39	2	PQ0011	tubulin beta chain
412	3	8.8	39	2	S63482	tubulin beta chain

413	3	8.8	39	2	G64944	yebJ protein - Esc
414	3	8.8	39	2	A85795	hypothetical prote
415	3	8.8	39	2	S78008	fucosyltransferase
416	3	8.8	39	2	JQ0282	hypothetical 4.3K
417	3	8.8	39	2	A48110	RNA recognition mo
418	3	8.8	39	2	H95146	hypothetical prote
419	3	8.8	39	2	D70239	hypothetical prote
420	3	8.8	39	2	G81899	hypothetical prote
421	3	8.8	39	2	B81912	hypothetical prote
422	3	8.8	39	2	B81954	very hypothetical
423	3	8.8	39	2	F82329	hypothetical prote
424	3	8.8	39	2	A43591	43K outer membrane
425	3	8.8	39	2	A44918	lactococcin G pept
426	3	8.8	39	2	S67938	hypothetical prote
427	3	8.8	39	2	S73118	photosystem II pro
428	3	8.8	39	2	PC4294	high mobility grou
429	3	8.8	39	2	T15158	hypothetical prote
430	3	8.8	39	2	I46466	luteinizing hormon
431	3	8.8	39	2	B40984	finger protein zfe
432	3	8.8	39	2	T03365	gene e2 protein -
433	3	8.8	39	2	F81587	hypothetical prote
434	3	8.8	39	2	E81540	hypothetical prote
435	3	8.8	39	2	T12905	hypothetical prote
436	3	8.8	39	2	AD0162	hypothetical prote
437	3	8.8	39	2	AE3109	hypothetical prote
438	3	8.8	40	1	SWFGS	sauvagine - Sauvag
439	3	8.8	40	2	B61320	plastocyanin - Aqu
440	3	8.8	40	2	S00264	creatine kinase (E
441	3	8.8	40	2	S34407	adenylate kinase (
442	3	8.8	40	2	PQ0202	endo-1,4-beta-xyla
443	3	8.8	40	2	S50021	trypsin-like prote
444	3	8.8	40	2	B60908	beta-lactamase (EC
445	3	8.8	40	2	B41440	protein disulfide-
446	3	8.8	40	2	A19940	antithrombin III -
447	3	8.8	40	2	B59005	thymosin beta - sc
448	3	8.8	40	2	A59005	thymosin beta - se
449	3	8.8	40	2	S07969	T-cell receptor al
450	3	8.8	40	2	I50012	MHC class I protei
451	3	8.8	40	2	I50013	MHC class I protei
452	3	8.8	40	2	S61539	ribosomal protein
453	3	8.8	40	2	A60171	proteoglycan core
454	3	8.8	40	2	A60645	tubulin beta chain
455	3	8.8	40	2	A29184	vitellogenin - tur
456	3	8.8	40	2	S65907	conglutin gamma -
457	3	8.8	40	2	S08656	protein VI - human
458	3	8.8	40	2	T08107	nonenzymatic prote
459	3	8.8	40	2	S71917	hemoglobin, extrac
460	3	8.8	40	2	S58853	homeotic protein u
461	3	8.8	40	2	H95063	hypothetical prote
462	3	8.8	40	2	H91281	hypothetical prote
463	3	8.8	40	2	A87642	hypothetical prote
464	3	8.8	40	2	F87419	hypothetical prote
465	3	8.8	40	2	C32338	hypothetical 4K pr
466	3	8.8	40	2	C72398	hypothetical prote
467	3	8.8	40	2	S44935	hypothetical prote
468	3	8.8	40	2	A82203	hypothetical prote
469	3	8.8	40	2	G82484	hypothetical prote

470	3	8.8	40	2	A82382	hypothetical prote
471	3	8.8	40	2	I39944	regulatory extrace
472	3	8.8	40	2	F69677	phosphatase (RapK)
473	3	8.8	40	2	I41476	probable antigen 9
474	3	8.8	40	2	S27709	hypothetical prote
475	3	8.8	40	2	F45095	photosystem I ligh
476	3	8.8	40	2	T11811	hypothetical prote
477	3	8.8	40	2	T07472	hypothetical prote
478	3	8.8	40	2	T07516	hypothetical prote
479	3	8.8	40	2	T07523	hypothetical prote
480	3	8.8	40	2	T07560	hypothetical prote
481	3	8.8	40	2	T48629	hypothetical prote
482	3	8.8	40	2	S53001	mitotic-specific c
483	3	8.8	40	2	T03831	hypothetical prote
484	3	8.8	40	2	S71295	deoxyguanosine kin
485	3	8.8	40	2	S56768	capsid protein - L
486	3	8.8	40	2	T07206	hypothetical prote
487	3	8.8	40	2	H81592	hypothetical prote
488	3	8.8	40	2	H81520	hypothetical prote
489	3	8.8	40	2	F81511	hypothetical prote
490	3	8.8	40	2	G82620	hypothetical prote
491	3	8.8	40	2	A82590	hypothetical prote
492	3	8.8	40	2	A86123	hypothetical prote
493	3	8.8	40	2	B97413	hypothetical prote
494	2	5.9	28	1	LFSEW	trp operon leader
495	2	5.9	28	1	LFEBLT	leu operon leader
496	2	5.9	28	1	G9BPSV	gene 9 protein - s
497	2	5.9	28	2	S41774	ubiquinol-cytochro
498	2	5.9	28	2	S04341	cytochrome P450 PB
499	2	5.9	28	2	PX0033	cytochrome P450 te
500	2	5.9	28	2	S66436	allophycocyanin al
501	2	5.9	28	2	S47624	D-aspartate oxidas
502	2	5.9	28	2	T14210	NADH2 dehydrogenas
503	2	5.9	28	2	T14213	NADH2 dehydrogenas
504	2	5.9	28	2	T12301	NADH2 dehydrogenas
505	2	5.9	28	2	PC1162	cytochrome-c oxida
506	2	5.9	28	2	S21278	glutathione transf
507	2	5.9	28	2	C33948	glutathione transf
508	2	5.9	28	2	A34244	hexokinase (EC 2.7
509	2	5.9	28	2	D38578	protein kinase 4 (
510	2	5.9	28	2	B39116	epidermal growth f
511	2	5.9	28	2	A31859	deoxycytidine kina
512	2	5.9	28	2	B54257	deoxynucleoside ki
513	2	5.9	28	2	I55596	lysosomal acid lip
514	2	5.9	28	2	B35948	phospholipase A2 (
515	2	5.9	28	2	C35948	phospholipase A2 (
516	2	5.9	28	2	A35115	hypothetical prote
517	2	5.9	28	2	A61281	lysozyme homolog A
518	2	5.9	28	2	A61529	chymotrypsin (EC 3
519	2	5.9	28	2	A60291	24K proteinase (EC
520	2	5.9	28	2	S08186	proteasome beta ch
521	2	5.9	28	2	S55729	orotidine-5'-monop
522	2	5.9	28	2	I40034	trpE protein - Bac
523	2	5.9	28	2	A32643	deoxyribodipyrimid
524	2	5.9	28	2	S77854	glutamate-tRNA lig
525	2	5.9	28	2	S07156	trypsin inhibitor
526	2	5.9	28	2	B45041	trypsin inhibitor

527	2	5.9	28	2	A25802	2S seed storage pr
528	2	5.9	28	2	T47196	RAS protein [impor
529	2	5.9	28	2	A61322	somatostatin-28 -
530	2	5.9	28	2	B60583	glycoprotein hormo
531	2	5.9	28	2	A38232	vasoactive intesti
532	2	5.9	28	2	A60303	vasoactive intesti
533	2	5.9	28	2	JT0412	bombyxin-IV chain
534	2	5.9	28	2	C44180	alpha-neurotoxin-1
535	2	5.9	28	2	C39327	long neurotoxin -
536	2	5.9	28	2	I32529	Ig lambda chain V
537	2	5.9	28	2	S58386	T-cell receptor be
538	2	5.9	28	2	PC1001	Ig light chain V r
539	2	5.9	28	2	B47719	T-cell receptor al
540	2	5.9	28	2	D47719	T-cell receptor al
541	2	5.9	28	2	S58389	T-cell receptor be
542	2	5.9	28	2	PH0250	T-cell receptor Vb
543	2	5.9	28	2	PH0247	T-cell receptor Vb
544	2	5.9	28	2	A49829	T-cell receptor va
545	2	5.9	28	2	D49829	T-cell receptor va
546	2	5.9	28	2	PH1908	T-cell receptor al
547	2	5.9	28	2	D41912	T-cell receptor be
548	2	5.9	28	2	G47719	house-dust-mite-re
549	2	5.9	28	2	E49533	T-cell receptor be
550	2	5.9	28	2	I46921	gene Bota protein
551	2	5.9	28	2	S11618	ribosomal protein
552	2	5.9	28	2	S51060	ribosomal protein
553	2	5.9	28	2	S51067	ribosomal protein
554	2	5.9	28	2	S72460	ribosomal protein
555	2	5.9	28	2	S08569	ribosomal protein
556	2	5.9	28	2	S10052	ribosomal protein
557	2	5.9	28	2	S55442	beta A2 crystallin
558	2	5.9	28	2	A45626	beta 2-tubulin - n
559	2	5.9	28	2	S21231	calcium-binding pr
560	2	5.9	28	2	A23691	apolipoprotein C-I
561	2	5.9	28	2	A05296	fibrinogen alpha c
562	2	5.9	28	2	A61113	cellular retinol-b
563	2	5.9	28	2	B35577	cell adhesion rece
564	2	5.9	28	2	I48349	fibronectin - mous
565	2	5.9	28	2	A61233	retinol-binding pr
566	2	5.9	28	2	I45911	dnaK-type molecula
567	2	5.9	28	2	PQ0263	dnaK-type molecula
568	2	5.9	28	2	A03356	omega-gliadin - ei
569	2	5.9	28	2	A60359	pollen allergen DG
570	2	5.9	28	2	A60752	outer membrane pro
571	2	5.9	28	2	PQ0691	photosystem I 5.6K
572	2	5.9	28	2	G32351	34K class B flagel
573	2	5.9	28	2	S47614	zinc finger protei
574	2	5.9	28	2	S49924	stp protein (Baker
575	2	5.9	28	2	B39227	calcium channel pr
576	2	5.9	28	2	F54346	pyruvate synthase
577	2	5.9	28	2	A36153	major allergen Ole
578	2	5.9	28	2	B54127	dolichyl-diphospha
579	2	5.9	28	2	S56746	alpha-synuclein, N
580	2	5.9	28	2	I48178	orphan receptor -
581	2	5.9	28	2	PC4429	peroxisome prolife
582	2	5.9	28	2	PC4430	peroxisome prolife
583	2	5.9	28	2	S29135	aminopyrine N-deme

584	2	5.9	28	2	S29136	aminopyrine N-deme
585	2	5.9	28	2	PN0625	homeobox JRX prote
586	2	5.9	28	2	B56779	tetM 5'-region lea
587	2	5.9	28	2	JU0297	fruR-shl operon le
588	2	5.9	28	2	C90639	fruR leader peptid
589	2	5.9	28	2	B47310	MHVS28AA - murine
590	2	5.9	28	2	E64656	hypothetical prote
591	2	5.9	28	2	B64669	hypothetical prote
592	2	5.9	28	2	S15235	hypothetical prote
593	2	5.9	28	2	S29285	arylalkyl acylamid
594	2	5.9	28	2	C56262	uvrB 3'-region hyp
595	2	5.9	28	2	E81239	hypothetical prote
596	2	5.9	28	2	I60364	phosphorybosylpyro
597	2	5.9	28	2	B39191	hypothetical prote
598	2	5.9	28	2	T17391	hypothetical prote
599	2	5.9	28	2	A56499	brevicin-27 - Lact
600	2	5.9	28	2	A41476	probable antigen 1
601	2	5.9	28	2	S16228	aryl acylamidase -
602	2	5.9	28	2	T37143	hypothetical prote
603	2	5.9	28	2	PS0106	2-phosphinomethylm
604	2	5.9	28	2	G69384	conserved hypothet
605	2	5.9	28	2	A69259	hypothetical prote
606	2	5.9	28	2	T06925	hypothetical prote
607	2	5.9	28	2	S38524	rRNA N-glycosidase
608	2	5.9	28	2	S21742	3-oxoacyl-[acyl-ca
609	2	5.9	28	2	PQ0800	calmodulin antagon
610	2	5.9	28	2	T06340	ribosomal protein
611	2	5.9	28	2	T07599	hypothetical prote
612	2	5.9	28	2	PH0220	peroxidase (EC 1.1
613	2	5.9	28	2	JQ0272	hypothetical 3K pr
614	2	5.9	28	2	S46250	fatty-acid-binding
615	2	5.9	28	2	A44923	carboxypeptidase 3
616	2	5.9	28	2	S64701	hypothetical prote
617	2	5.9	28	2	T38041	similarity to yeas
618	2	5.9	28	2	A60698	trichocyst protein
619	2	5.9	28	2	A61417	bdellin B-3 - medi
620	2	5.9	28	2	S06668	toxin-like protein
621	2	5.9	28	2	S07826	venom protein - Am
622	2	5.9	28	2	C34923	omega-agatoxin IIA
623	2	5.9	28	2	A44877	cell surface prote
624	2	5.9	28	2	JW0019	mast cell degranul
625	2	5.9	28	2	A61273	interleukin-1 - st
626	2	5.9	28	2	S68643	nicotinic acetylch
627	2	5.9	28	2	PC2162	angiotensin II rec
628	2	5.9	28	2	I54183	cell adhesion regu
629	2	5.9	28	2	S54338	cytochrome P450 CY
630	2	5.9	28	2	I52627	erythrocyte chemok
631	2	5.9	28	2	JQ1035	hypothetical 3.2K
632	2	5.9	28	2	PH1335	Ig heavy chain DJ
633	2	5.9	28	2	S37683	protein IEF SSP 91
634	2	5.9	28	2	S37686	protein IEF SSP 92
635	2	5.9	28	2	PH1911	T-cell receptor al
636	2	5.9	28	2	I39288	ZF3 domain - human
637	2	5.9	28	2	PL0005	pepsin A (EC 3.4.2
638	2	5.9	28	2	A60692	proline-rich prote
639	2	5.9	28	2	PC2239	heat shock protein
640	2	5.9	28	2	PT0366	T-cell receptor be

641	2	5.9	28	2	I58115	cystic fibrosis tr
642	2	5.9	28	2	A46690	sialic acid-specif
643	2	5.9	28	2	C83797	hypothetical prote
644	2	5.9	28	2	C83969	hypothetical prote
645	2	5.9	28	2	S51593	myrB protein - Mic
646	2	5.9	28	2	C85490	fruR leader peptid
647	2	5.9	28	2	C97078	hypothetical prote
648	2	5.9	28	2	F97000	hypothetical prote
649	2	5.9	28	2	AB1093	hypothetical prote
650	2	5.9	28	2	T06490	probable ribulose-
651	2	5.9	28	2	S73563	H+-transporting tw
652	2	5.9	28	2	AG0516	leu operon leader
653	2	5.9	28	4	I68614	frame shifted FMR1
654	2	5.9	28	4	JN0014	GABA(A) receptor a
655	2	5.9	29	1	TIPU	trypsin inhibitor
656	2	5.9	29	1	TIPU3	trypsin inhibitor
657	2	5.9	29	1	TIPU2B	trypsin inhibitor
658	2	5.9	29	1	GCOPV	glucagon - North A
659	2	5.9	29	1	GCDK	glucagon - duck
660	2	5.9	29	1	A61583	glucagon - ostrich
661	2	5.9	29	1	GCFLE	glucagon - Europea
662	2	5.9	29	1	GCDF	glucagon - smaller
663	2	5.9	29	1	GCEN	glucagon - elephan
664	2	5.9	29	1	GCTTS	glucagon - slider
665	2	5.9	29	1	TNLJBR	trans-activating t
666	2	5.9	29	1	Q1BP57	gene 1.5 protein -
667	2	5.9	29	2	A60558	cytochrome P450 HL
668	2	5.9	29	2	T17079	NADH2 dehydrogenas
669	2	5.9	29	2	T17076	NADH2 dehydrogenas
670	2	5.9	29	2	A48427	flavohemoglobin hm
671	2	5.9	29	2	A54234	cytochrome-c oxida
672	2	5.9	29	2	S08201	peroxidase (EC 1.1
673	2	5.9	29	2	S39968	probable hydro-lya
674	2	5.9	29	2	A26208	acetyl-CoA C-acety
675	2	5.9	29	2	A22018	phosphotransferase
676	2	5.9	29	2	S46211	kallikrein rK8 (pK
677	2	5.9	29	2	S28174	heat-shock protein
678	2	5.9	29	2	A32414	bothrolysin (EC 3.
679	2	5.9	29	2	S17432	H+-transporting tw
680	2	5.9	29	2	S02578	H+-transporting tw
681	2	5.9	29	2	S23122	peptidylprolyl iso
682	2	5.9	29	2	JU0211	squash-type trypsi
683	2	5.9	29	2	T03653	phospholipid trans
684	2	5.9	29	2	C24536	alpha-amylase/tryp
685	2	5.9	29	2	C25310	alpha-amylase/tryp
686	2	5.9	29	2	D55998	brevinin-2Ed - edi
687	2	5.9	29	2	D53578	brevinin-2Ee - edi
688	2	5.9	29	2	A91740	glucagon - turkey
689	2	5.9	29	2	A91741	glucagon - rabbit
690	2	5.9	29	2	A91742	glucagon - Arabian
691	2	5.9	29	2	S07211	glucagon - marbled
692	2	5.9	29	2	A61135	glucagon - bigeye
693	2	5.9	29	2	C39258	glucagon - common
694	2	5.9	29	2	C60840	glucagon I - Europ
695	2	5.9	29	2	S39018	glucagon - bowfin
696	2	5.9	29	2	A39462	cholestokinin - do
697	2	5.9	29	2	A60791	toxin II.9 - scorp

698	2	5.9	29	2	A43620	omega-conotoxin GV
699	2	5.9	29	2	B43620	omega-conotoxin GV
700	2	5.9	29	2	JH0699	omega-conotoxin MV
701	2	5.9	29	2	A58537	omega-conotoxin MV
702	2	5.9	29	2	C61233	conceptus protein
703	2	5.9	29	2	S10061	Ig heavy chain (cl
704	2	5.9	29	2	PH1328	Ig heavy chain DJ
705	2	5.9	29	2	PH0239	T-cell receptor Vb
706	2	5.9	29	2	PH0251	T-cell receptor Vb
707	2	5.9	29	2	PH0254	T-cell receptor Vb
708	2	5.9	29	2	PH0233	T-cell receptor Vb
709	2	5.9	29	2	E31485	Ig heavy chain V r
710	2	5.9	29	2	H31485	Ig kappa chain V r
711	2	5.9	29	2	G31461	T-cell receptor de
712	2	5.9	29	2	C47719	T-cell receptor al
713	2	5.9	29	2	E47719	house-dust-mite-re
714	2	5.9	29	2	PS0134	H-2 class I histoc
715	2	5.9	29	2	PS0132	H-2 class I histoc
716	2	5.9	29	2	D32533	class II histocomp
717	2	5.9	29	2	I37534	gene HLA-DRB prote
718	2	5.9	29	2	I37535	gene HLA-DRB prote
719	2	5.9	29	2	I37536	MHC class II histo
720	2	5.9	29	2	I37301	MHC class II histo
721	2	5.9	29	2	I37303	HLA-DR beta - huma
722	2	5.9	29	2	I37306	HLA-DR beta - huma
723	2	5.9	29	2	I50214	protein-tyrosine-p
724	2	5.9	29	2	S07771	histone H2B.2, spe
725	2	5.9	29	2	T04412	histone H3 - barle
726	2	5.9	29	2	T44245	ribosomal protein
727	2	5.9	29	2	S51070	ribosomal protein
728	2	5.9	29	2	S08555	ribosomal protein
729	2	5.9	29	2	PC4231	ribosomal protein
730	2	5.9	29	2	S10050	ribosomal protein
731	2	5.9	29	2	S10049	ribosomal protein
732	2	5.9	29	2	S26229	ribosomal protein
733	2	5.9	29	2	A27561	Meth A tumor-speci
734	2	5.9	29	2	S10725	calmodulin-binding
735	2	5.9	29	2	E33208	calreticulin, uter
736	2	5.9	29	2	C33208	calreticulin, slow
737	2	5.9	29	2	D33208	calreticulin, brai
738	2	5.9	29	2	A45474	thrombospondin 2 -
739	2	5.9	29	2	G39690	neural cell adhesi
740	2	5.9	29	2	A61166	endometrial proges
741	2	5.9	29	2	I52402	alpha-fetoprotein
742	2	5.9	29	2	S00564	enamel protein - r
743	2	5.9	29	2	S57232	homeotic protein s
744	2	5.9	29	2	S06854	chorion class B pr
745	2	5.9	29	2	A43038	auxin-binding prot
746	2	5.9	29	2	T12082	proline-rich prote
747	2	5.9	29	2	S70328	gamma35 secalin -
748	2	5.9	29	2	S29208	avenin gamma-3 - o
749	2	5.9	29	2	S07055	photosystem I prot
750	2	5.9	29	2	S08088	gene VII protein -
751	2	5.9	29	2	F42075	finger protein (cl
752	2	5.9	29	2	T51116	probable precorrin
753	2	5.9	29	2	A53145	high conductance c
754	2	5.9	29	2	A35121	hypothetical prote

755	2	5.9	29	2	S03277	photosystem II 5K
756	2	5.9	29	2	S63509	glycine reductase
757	2	5.9	29	2	A55891	delta-conotoxin Gm
758	2	5.9	29	2	S32730	homeotic protein -
759	2	5.9	29	2	S57225	labial protein (cl
760	2	5.9	29	2	S32732	homeotic protein -
761	2	5.9	29	2	S32734	homeotic protein -
762	2	5.9	29	2	S32733	homeotic protein -
763	2	5.9	29	2	G90719	hypothetical prote
764	2	5.9	29	2	S07513	gene 5.1 protein -
765	2	5.9	29	2	S14040	hypothetical prote
766	2	5.9	29	2	E64586	hypothetical prote
767	2	5.9	29	2	B64607	hypothetical prote
768	2	5.9	29	2	G64674	hypothetical prote
769	2	5.9	29	2	G83440	KdpF protein PA163
770	2	5.9	29	2	A49288	alcohol dehydrogen
771	2	5.9	29	2	A81078	hypothetical prote
772	2	5.9	29	2	B81006	hypothetical prote
773	2	5.9	29	2	T48910	KdpF protein [vali
774	2	5.9	29	2	A35445	repY protein - Esc
775	2	5.9	29	2	S19943	aadB protein - Kle
776	2	5.9	29	2	A49914	S-layer protein va
777	2	5.9	29	2	E64036	hypothetical prote
778	2	5.9	29	2	B48363	2-hydroxyglutaryl-
779	2	5.9	29	2	C40638	orf 3' of cycI - R
780	2	5.9	29	2	S05224	photosystem I 4.8K
781	2	5.9	29	2	B56817	photosystem I chai
782	2	5.9	29	2	S74572	hypothetical prote
783	2	5.9	29	2	C60743	putrescine carbamo
784	2	5.9	29	2	S67989	HA-19/HA-52 protei
785	2	5.9	29	2	S14099	12-alpha-hydroxyst
786	2	5.9	29	2	S77569	plantaricin SA6 -
787	2	5.9	29	2	S21222	48K protein - Euba
788	2	5.9	29	2	S03947	hydrogen dehydroge
789	2	5.9	29	2	T34643	hypothetical prote
790	2	5.9	29	2	T37120	hypothetical prote
791	2	5.9	29	2	T36654	probable small mem
792	2	5.9	29	2	B43937	endo-1,4-beta-xyla
793	2	5.9	29	2	S09556	hypothetical prote
794	2	5.9	29	2	T06904	hypothetical prote
795	2	5.9	29	2	S73197	hypothetical prote
796	2	5.9	29	2	S78326	conserved hypothet
797	2	5.9	29	2	S78310	hypothetical prote
798	2	5.9	29	2	S78360	hypothetical prote
799	2	5.9	29	2	S01572	hypothetical prote
800	2	5.9	29	2	T07450	hypothetical prote
801	2	5.9	29	2	S01448	hypothetical prote
802	2	5.9	29	2	S38525	rRNA N-glycosidase
803	2	5.9	29	2	T52557	translation elonga
804	2	5.9	29	2	PQ0862	allantoinase (EC 3
805	2	5.9	29	2	PQ0486	globulin 2a - taro
806	2	5.9	29	2	S02200	prolamin alpha-1 -
807	2	5.9	29	2	A60683	malate dehydrogena
808	2	5.9	29	2	JQ0212	hypothetical 3K pr
809	2	5.9	29	2	S58541	hypothetical prote
810	2	5.9	29	2	PC2035	alanine transamina
811	2	5.9	29	2	B21112	variant surface gl

812	2	5.9	29	2	C60110	repetitive protein
813	2	5.9	29	2	D24802	cuticle protein 36
814	2	5.9	29	2	A56591	E75 steroid recept
815	2	5.9	29	2	A61613	ceratotoxin A - Me
816	2	5.9	29	2	B61613	ceratotoxin B - Me
817	2	5.9	29	2	PH1230	lectin - namazu (f
818	2	5.9	29	2	A32860	biotin-binding pro
819	2	5.9	29	2	I50382	c-mil protein - ch
820	2	5.9	29	2	I50695	non-collagenous al
821	2	5.9	29	2	B54197	70k thyroid autoan
822	2	5.9	29	2	A35891	carcinoembryonic a
823	2	5.9	29	2	I77372	CD44SP - human
824	2	5.9	29	2	S54340	diazepam binding i
825	2	5.9	29	2	A41683	hyaluronate recept
826	2	5.9	29	2	C54037	splicing regulator
827	2	5.9	29	2	S35924	T-cell receptor ga
828	2	5.9	29	2	C61384	trachael mucin gly
829	2	5.9	29	2	A60604	glutathione peroxi
830	2	5.9	29	2	S57204	oviduct-specific s
831	2	5.9	29	2	I47025	antigen WC1 [impor
832	2	5.9	29	2	A49410	t-complex polypept
833	2	5.9	29	2	PS0125	H-2 class I histoc
834	2	5.9	29	2	S46929	teg169 protein - m
835	2	5.9	29	2	S38749	vimentin homolog -
836	2	5.9	29	2	S42764	Ca2+/calmodulin-de
837	2	5.9	29	2	A49708	synaptosomal-assoc
838	2	5.9	29	2	H83777	hypothetical prote
839	2	5.9	29	2	C83833	hypothetical prote
840	2	5.9	29	2	F83870	hypothetical prote
841	2	5.9	29	2	B84144	hypothetical prote
842	2	5.9	29	2	PC4421	multactivase (EC 3
843	2	5.9	29	2	B85840	hypothetical prote
844	2	5.9	29	2	C85840	hypothetical prote
845	2	5.9	29	2	G86058	hypothetical prote
846	2	5.9	29	2	E89904	hypothetical prote
847	2	5.9	29	2	H89949	hypothetical prote
848	2	5.9	29	2	A59278	neurotoxin BmK A3-
849	2	5.9	29	2	S17496	inorganic diphosph
850	2	5.9	29	2	PQ0782	NADH2 dehydrogenas
851	2	5.9	29	2	S34762	L-serine ammonia-l
852	2	5.9	29	2	AB0717	hypothetical prote
853	2	5.9	29	2	AC0717	hypothetical prote
854	2	5.9	29	2	AH2338	PetN protein [impo
855	2	5.9	29	4	I58970	hypothetical prote
856	2	5.9	30	1	AIBSAF	thermophilic amino
857	2	5.9	30	1	TIPU1W	trypsin inhibitor
858	2	5.9	30	1	IRTRC3	protamine CIII, ma
859	2	5.9	30	1	IRTR78	protamine CIII, mi
860	2	5.9	30	1	IRTR4	protamine pTP4 - r
861	2	5.9	30	1	SNUMP	sillucin - Rhizomu
862	2	5.9	30	2	I57689	ubiquinol-cytochro
863	2	5.9	30	2	I52254	gene CYP11B2 prote
864	2	5.9	30	2	B56859	fatty acid omega-h
865	2	5.9	30	2	A27375	photosystem I iron
866	2	5.9	30	2	F60691	phycobilisome beta
867	2	5.9	30	2	S11131	NADH2 dehydrogenas
868	2	5.9	30	2	S14214	NADH2 dehydrogenas

869	2	5.9	30	2	S08202	peroxidase (EC 1.1
870	2	5.9	30	2	S08204	peroxidase (EC 1.1
871	2	5.9	30	2	S08203	peroxidase (EC 1.1
872	2	5.9	30	2	A39089	hydrogenase (EC 1.
873	2	5.9	30	2	I38066	nitric-oxide synth
874	2	5.9	30	2	I39799	CAT-66 - Bacillus
875	2	5.9	30	2	A18780	dimethylallyltrans
876	2	5.9	30	2	S03283	methionine adenosy
877	2	5.9	30	2	S71865	glutathione transf
878	2	5.9	30	2	B27103	aspartate transami
879	2	5.9	30	2	A27103	aspartate transami
880	2	5.9	30	2	I55427	aspartate transami
881	2	5.9	30	2	A49955	protein-tyrosine k
882	2	5.9	30	2	S68639	nigroxin A - black
883	2	5.9	30	2	S68640	nigroxin B - black
884	2	5.9	30	2	D57001	endo-1,4-beta-xyla
885	2	5.9	30	2	A43937	endo-1,4-beta-xyla
886	2	5.9	30	2	PC2361	alpha-glucosidase
887	2	5.9	30	2	PX0073	epoxide hydrolase
888	2	5.9	30	2	B60291	30K serine protein
889	2	5.9	30	2	A27634	major fecal allerg
890	2	5.9	30	2	B27634	major fecal allerg
891	2	5.9	30	2	I77411	renin-2 - mouse (f
892	2	5.9	30	2	PC2328	proteasome endopep
893	2	5.9	30	2	A34486	inorganic diphosph
894	2	5.9	30	2	S21816	H+-exporting ATPas
895	2	5.9	30	2	S21814	H+-exporting ATPas
896	2	5.9	30	2	S21815	H+-exporting ATPas
897	2	5.9	30	2	S74121	fructose-bisphosph
898	2	5.9	30	2	S25666	phosphopyruvate hy
899	2	5.9	30	2	S69600	peptidylprolyl iso
900	2	5.9	30	2	A60517	alpha-1-antitrypsi
901	2	5.9	30	2	S24979	proteinase inhibit
902	2	5.9	30	2	JX0057	trypsin inhibitor
903	2	5.9	30	2	JS0579	squash-type trypsi
904	2	5.9	30	2	JQ1958	trypsin inhibitor
905	2	5.9	30	2	PC1113	proteinase inhibit
906	2	5.9	30	2	C42842	antifungal 2S stor
907	2	5.9	30	2	S70341	napin large chain
908	2	5.9	30	2	S70343	napin large chain
909	2	5.9	30	2	A33308	thrombomodulin - r
910	2	5.9	30	2	A61130	somatotropin - Ame
911	2	5.9	30	2	S44473	glucagon-like pept
912	2	5.9	30	2	A59076	defensin alpha-1 -
913	2	5.9	30	2	B59076	defensin alpha-2 -
914	2	5.9	30	2	B60791	toxin II.6 - scorp
915	2	5.9	30	2	A31187	neurotoxin II.22.5
916	2	5.9	30	2	I68109	interferon alpha-W
917	2	5.9	30	2	C49533	T-cell receptor al
918	2	5.9	30	2	S20778	Ig heavy chain V r
919	2	5.9	30	2	PL0092	Ig heavy chain V r
920	2	5.9	30	2	PH0245	T-cell receptor Vb
921	2	5.9	30	2	PH0228	T-cell receptor Vb
922	2	5.9	30	2	PH0252	T-cell receptor Vb
923	2	5.9	30	2	PH0882	Ig kappa chain V r
924	2	5.9	30	2	E31461	T-cell receptor de
925	2	5.9	30	2	F32502	T-cell receptor de

926	2	5.9	30	2	PH0235	T-cell receptor Vb
927	2	5.9	30	2	A49533	T-cell receptor al
928	2	5.9	30	2	C27579	T-cell receptor be
929	2	5.9	30	2	I37626	Fc gamma (IgG) rec
930	2	5.9	30	2	PS0121	H-2 class I histoc
931	2	5.9	30	2	S74192	crotoxin inhibitor
932	2	5.9	30	2	A05253	hemoglobin epsilon
933	2	5.9	30	2	A21680	hemoglobin epsilon
934	2	5.9	30	2	A05254	hemoglobin epsilon
935	2	5.9	30	2	S68618	histone H2B - sea
936	2	5.9	30	2	PD0014	cAMP response elem
937	2	5.9	30	2	PN0651	restriction endonu
938	2	5.9	30	2	S11613	ribosomal protein
939	2	5.9	30	2	A60511	gamma-crystallin -
940	2	5.9	30	2	I49412	gamma-crystallin-3
941	2	5.9	30	2	S12965	gamma-crystallin -
942	2	5.9	30	2	S69269	ezrin homolog - bo
943	2	5.9	30	2	A61189	tubulin beta chain
944	2	5.9	30	2	I52806	Duchenne muscular
945	2	5.9	30	2	S21153	calcium-binding pr
946	2	5.9	30	2	A26188	lipocortin I - pig
947	2	5.9	30	2	A56790	annexin, isoform P
948	2	5.9	30	2	A34622	fibrinogen beta ch
949	2	5.9	30	2	A03148	retinol-binding pr
950	2	5.9	30	2	A48299	taurine transporte
951	2	5.9	30	2	B61511	serum albumin, mil
952	2	5.9	30	2	B39819	neutrophil chemota
953	2	5.9	30	2	A38933	vitronectin - bovi
954	2	5.9	30	2	S57234	fushi tarazu segme
955	2	5.9	30	2	S69124	rRNA N-glycosidase
956	2	5.9	30	2	S69125	rRNA N-glycosidase
957	2	5.9	30	2	S07065	rRNA N-glycosidase
958	2	5.9	30	2	A31836	17K antigen - Rick
959	2	5.9	30	2	PQ0669	photosystem I 17.5
960	2	5.9	30	2	E45095	photosystem I ligh
961	2	5.9	30	2	B45095	photosystem I ligh
962	2	5.9	30	2	B24987	regulatory protein
963	2	5.9	30	2	S30757	genome polyprotein
964	2	5.9	30	2	S30760	genome polyprotein
965	2	5.9	30	2	S30759	genome polyprotein
966	2	5.9	30	2	B44314	intracisternal A p
967	2	5.9	30	2	S13753	replication initia
968	2	5.9	30	2	S26175	tail tubular prote
969	2	5.9	30	2	S69352	N-methylhydantoin
970	2	5.9	30	2	S68312	glucuronosyltransf
971	2	5.9	30	2	PH1228	D-aminoacylase (EC
972	2	5.9	30	2	S42364	aromatic-amino-aci
973	2	5.9	30	2	S05223	photosystem I 6.5K
974	2	5.9	30	2	S30333	N-carbamoyl-D-amin
975	2	5.9	30	2	S28991	antifungal protein
976	2	5.9	30	2	PC2307	X-Pro aminopeptida
977	2	5.9	30	2	PQ0484	globulin lb - taro
978	2	5.9	30	2	C43591	51K outer membrane
979	2	5.9	30	2	B43591	45K outer membrane
980	2	5.9	30	2	S06411	killer plasmid 28K
981	2	5.9	30	2	B49292	GDP dissociation i
982	2	5.9	30	2	A60914	pheromone-binding

983	2	5.9	30	2	PS0437	potassium channel
984	2	5.9	30	2	PS0438	potassium channel
985	2	5.9	30	2	A47607	immunogenic protei
986	2	5.9	30	2	S02088	blood group Rh-rel
987	2	5.9	30	2	S57227	proboscipedia prot
988	2	5.9	30	2	H95008	hypothetical prote
989	2	5.9	30	2	C95030	hypothetical prote
990	2	5.9	30	2	G95031	hypothetical prote
991	2	5.9	30	2	E95079	hypothetical prote
992	2	5.9	30	2	F95118	hypothetical prote
993	2	5.9	30	2	E95145	hypothetical prote
994	2	5.9	30	2	F89406	protein R10E8.7 [i
995	2	5.9	30	2	F87254	hypothetical prote
996	2	5.9	30	2	E84786	hypothetical prote
997	2	5.9	30	2	C84481	hypothetical prote
998	2	5.9	30	2	B47483	cysteine-rich para
999	2	5.9	30	2	S15141	hypothetical prote
1000	2	5.9	30	2	S13985	hypothetical prote

ALIGNMENTS

RESULT 1

A84241

hypothetical protein Vng0840h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84241

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welte, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.; Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich, J.L.; Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: A84241

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <STO>

A;Cross-references: GB:AE004437; NID:g10580410; PIDN:AAG19293.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG0840H

Query Match 14.7%; Score 5; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28
 |||||
 Db 26 LRKKL 30

RESULT 2

B97032

transcription regulator, AcrR family [imported] - *Clostridium acetobutylicum*

C;Species: *Clostridium acetobutylicum*

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C;Accession: B97032

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.; Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*.

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: B97032

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK79045.1; PID:g15023984; GSPDB:GN00168

A;Experimental source: *Clostridium acetobutylicum* ATCC824

C;Genetics:

A;Gene: CAC1071

Query Match 14.7%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
|||||
Db 30 SVSEI 34

RESULT 3

E95098

hypothetical protein SP0853 [imported] - *Streptococcus pneumoniae* (strain TIGR4)

C;Species: *Streptococcus pneumoniae*

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: E95098

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: E95098

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74982.1; PID:g14972326; GSPDB:GN00164; TIGR:SP4SP0853

A;Experimental source: strain TIGR4

C;Genetics:
A;Gene: SP0853

Query Match 14.7%; Score 5; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQD 30
|||||
Db 30 KKLQD 34

RESULT 4

T09594

gene LFY protein - Monterey pine (fragment)

C;Species: Pinus radiata (Monterey pine)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: T09594

R;Izquierdo, L.Y.; Vergara, R.F.; Alvarez-Buylla, E.R.

submitted to the EMBL Data Library, August 1996

A;Description: Partial characterization of Pinus radiata meristem identity
homolog gene (LFY).

A;Reference number: Z16756

A;Accession: T09594

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <IZQ>

A;Cross-references: EMBL:U66725; NID:g1513305; PID:g1513306

C;Genetics:

A;Gene: LFY

C;Function:

A;Description: controls meristem identity

Query Match 11.8%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||||
Db 15 LRKK 18

RESULT 5

A55527

pyrroloquinoline quinone precursor pqqD - Methylobacterium extorquens

C;Species: Methylobacterium extorquens

C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C;Accession: A55527

R;Morris, C.J.; Biville, F.; Turlin, E.; Lee, E.; Ellermann, K.; Fan, W.H.;

Ramamoorthi, R.; Springer, A.L.; Lidstrom, M.E.

J. Bacteriol. 176, 1746-1755, 1994

A;Title: Isolation, phenotypic characterization, and complementation analysis of
mutants of Methylobacterium extorquens AM1 unable to synthesize pyrroloquinoline
quinone and sequences of pqqD, pqqG, and pqqC.

A;Reference number: A55527; MUID:94179111; PMID:8132470

A;Accession: A55527

A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-29 <MOR>
A;Cross-references: GB:L25889; NID:g414589; PIDN:AAA17878.1; PID:g414590
C;Genetics:
A;Gene: pqqD
C;Superfamily: pyrroloquinoline quinone precursor pqqA
C;Keywords: quinoprotein
F;16,20/Product: pyrroloquinoline quinone #status predicted <MAT>
F;16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match 11.8%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
|||
Db 8 VSEI 11

RESULT 6

S01614

dystrophin - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C;Accession: S01614

R;Nudel, U.; Robzyk, K.; Yaffe, D.

Nature 331, 635-638, 1988

A;Title: Expression of the putative Duchenne muscular dystrophy gene in differentiated myogenic cell cultures and in the brain.

A;Reference number: S01614; MUID:88122671; PMID:3340214

A;Accession: S01614

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-29 <NUD>

A;Cross-references: EMBL:X07000; NID:g56137; PIDN:CAA30057.1; PID:g1334214

C;Genetics:

A;Map position: X

C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology;
spectrin/dystrophin repeat homology; WW repeat homology

C;Keywords: actin binding; cytoskeleton

Query Match 11.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
|||
Db 12 KLQD 15

RESULT 7

I78537

copper transporting P-type ATPase - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C;Accession: I78537

R;Thomas, G.R.; Forbes, J.R.; Roberts, E.A.; Walshe, J.M.; Cox, D.W.

Nature Genet. 9, 210-217, 1995

A;Title: The Wilson disease gene: spectrum of mutations and their consequences.

A;Reference number: I58128; MUID:95235569; PMID:7626145

A;Accession: I78537

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: GB:S77450; NID:g957354; PIDN:AAB34087.1; PID:g957355

C;Genetics:

A;Gene: GDB:ATP7B

A;Cross-references: GDB:120494; OMIM:277900

A;Map position: 13q14.3-13q21.1

Query Match 11.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEIQ 6
|||
Db 14 SEIQ 17

RESULT 8

S78412

ribosomal protein RL22/RL24, mitochondrial [validated] - rat (tentative sequence) (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000

C;Accession: S78412; S78413

R;Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A;Reference number: S78411

A;Accession: S78412

A;Molecule type: protein

A;Residues: 1-29 <GOL>

A;Note: the protein is designated as mitochondrial ribosomal protein L22

A;Accession: S78413

A;Molecule type: protein

A;Residues: 1-10,'XXP',14-15,'X',17-24 <GO2>

A;Note: the protein is designated as mitochondrial ribosomal protein L24

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 11.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 4 LRKK 7

RESULT 9

S01657

atrial natriuretic factor - laughing frog (tentative sequence) (fragment)

N;Alternate names: atriopeptin

C;Species: Rana ridibunda (laughing frog)

C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000

C;Accession: S01657; A30977
R;Lazure, C.; Ong, H.; McNicoll, N.; Netchitailo, P.; Chretien, M.; de Lean, A.; Vaudry, H.
FEBS Lett. 238, 300-306, 1988
A;Title: The amino acid sequences of frog heart atrial natriuretic-like peptide and mammalian ANF are closely related.
A;Reference number: S01657; MUID:89005705; PMID:2971573
A;Accession: S01657
A;Molecule type: protein
A;Residues: 1-30 <LAZ>
A;Note: the sequence from the summary is inconsistent with that from Fig. 3 in lacking residues 3-6
C;Superfamily: natriuretic peptide A precursor

Query Match 11.8%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 SMRR 20
|||
Db 4 SMRR 7

RESULT 10
S21195

spectrin beta chain - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C;Accession: S21195
R;Frappier, T.; Derancourt, J.; Pradel, L.A.
Eur. J. Biochem. 205, 85-91, 1992
A;Title: Actin and neurofilament binding domain of brain spectrin beta subunit.
A;Reference number: S21195; MUID:92209538; PMID:1555607
A;Accession: S21195
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-30 <FRA>
C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology;
spectrin/dystrophin repeat homology; WW repeat homology

Query Match 11.8%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 NSMR 19
|||
Db 19 NSMR 22

RESULT 11
S63531

hypothetical protein 1 - Sulfolobus solfataricus (fragment)
C;Species: Sulfolobus solfataricus
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S63531
R;Jones, C.E.; Fleming, T.M.; Cowan, D.A.; Littlechild, J.A.; Piper, P.W.
Eur. J. Biochem. 233, 800-808, 1995

A;Title: The phosphoglycerate kinase and glyceraldehyde-3-phosphate dehydrogenase genes from the thermophilic archaeon *Sulfolobus solfataricus* overlap by 8-bp: isolation, sequencing of the genes and expression in *Escherichia coli*.

A;Reference number: S63528; MUID:96085144; PMID:8521845

A;Accession: S63531

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-30 <JON>

A;Cross-references: EMBL:X80178

Query Match 11.8%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
 ||||
Db 11 WLRK 14

RESULT 12

S44471

glucagon G1 - North American paddlefish (*Polyodon spathula*)

C;Species: *Polyodon spathula*

C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 07-May-1999

C;Accession: S44471

R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (*Polyodon spathula*).

A;Reference number: S44467; MUID:94271144; PMID:8002937

A;Accession: S44471

A;Molecule type: protein

A;Residues: 1-31 <NGU>

A;Experimental source: pancreas

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

F;1-31/Product: glucagon G1 #status predicted <MAT>

Query Match 11.8%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24
 ||||
Db 23 VEWL 26

RESULT 13

S44472

glucagon G2 - North American paddlefish (*Polyodon spathula*)

C;Species: *Polyodon spathula*

C;Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 07-May-1999

C;Accession: S44472

R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (*Polyodon spathula*).
 A;Reference number: S44467; MUID:94271144; PMID:8002937
 A;Accession: S44472
 A;Molecule type: protein
 A;Residues: 1-31 <NGU>
 A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 5 in having 29-Glu
 C;Superfamily: glucagon
 C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas
 F;1-31/Product: glucagon G2 #status predicted <GCN>

Query Match 11.8%; Score 4; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24
 ||||
 Db 23 VEWL 26

RESULT 14

D70236

hypothetical protein BBH11 - Lyme disease spirochete plasmid H/lp28-3

C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C;Accession: D70236

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Wathney, L.; McDonald, L.; Artiach, P.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: D70236

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <KLE>

A;Cross-references: GB:AE000784; NID:g2690041; PIDN:AAC66002.1; PID:g2690058;

TIGR:BBH11

A;Experimental source: strain B31

C;Genetics:

A;Genome: plasmid

Query Match 11.8%; Score 4; DB 2; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 26 KKLQ 29

RESULT 15

F23454

ovalbumin phosphoserine peptide - fulvous whistling-duck (fragments)

C;Species: Dendrocygna bicolor (fulvous whistling-duck)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: F23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: F23454

A;Molecule type: protein

A;Residues: 1-32 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 26 SVSE 29

RESULT 16

G84161

hypothetical protein Vng0019h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: G84161

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welti, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.; Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich, J.L.; Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: G84161

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-32 <STO>

A;Cross-references: GB:AE004437; NID:g10579667; PIDN:AAG18659.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG0019H

Query Match 11.8%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
|||
Db 13 KLQD 16

RESULT 17

S22304

hypothetical protein - *Streptomyces coelicolor* (fragment)

C;Species: *Streptomyces coelicolor*

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Dec-1999

C;Accession: S22304; T42018

R;van Wezel, G.P.; Vijgenboom, E.; Bosch, L.

Nucleic Acids Res. 19, 4399-4403, 1991

A;Title: A comparative study of the ribosomal RNA operons of *Streptomyces coelicolor* A3(2) and sequence analysis of rrnA.

A;Reference number: S22304; MUID:91360338; PMID:1715981

A;Accession: S22304

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-32 <VAN>

A;Cross-references: EMBL:X60514; NID:g48948; PIDN:CAA43029.1; PID:g48949

A;Note: the authors translated the codon GAT for residue 8 as Asn, AGG for residue 16 as Ala, and CAG for residue 21 as Glu

Query Match 11.8%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 RRVE 22
 ||||
Db 15 RRVE 18

RESULT 18

E81714

hypothetical protein TC0337 [imported] - *Chlamydia muridarum* (strain Nigg)

C;Species: *Chlamydia muridarum*, *Chlamydia trachomatis* MoPn

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000

C;Accession: E81714

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.; Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser, C.M.

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: E81714

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-33 <TET>

A;Cross-references: GB:AE002301; GB:AE002160; NID:g7190372; PIDN:AAF39200.1; PID:g7190379; GSPDB:GN00121; TIGR:TC0337

A;Experimental source: strain Nigg (MoPn)

C;Genetics:

A;Gene: TC0337

Query Match 11.8%; Score 4; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
 ||||
Db 26 LRKK 29

RESULT 19

B97232

hypothetical protein CAC2698 [imported] - Clostridium acetobutylicum

C;Species: Clostridium acetobutylicum

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C;Accession: B97232

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.; Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum.

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: B97232

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK80645.1; PID:g15025731; GSPDB:GN00168

A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC2698

Query Match 11.8%; Score 4; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MRRV 21
 ||||
Db 19 MRRV 22

RESULT 20

D23454

ovalbumin phosphoserine peptide - golden pheasant (fragments)

C;Species: Chrysolophus pictus (golden pheasant)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: D23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: D23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 29 SVSE 32

RESULT 21

G23454

ovalbumin phosphoserine peptide - magpie goose (fragments)

C;Species: Anseranas semipalmata (magpie goose)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: G23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: G23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 29 SVSE 32

RESULT 22

B24677

Balbiani ring 2 chain (BR2.2) - midge (Chironomus pallidivittatus) (fragment)

C;Species: Chironomus pallidivittatus

C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 17-Mar-2000

C;Accession: B24677

R;Galler, R.; Saiga, H.; Widmer, R.M.; Lezzi, M.; Edstrom, J.E.

EMBO J. 4, 2977-2982, 1985

A;Title: Two genes in Balbiani ring 2 with metabolically different 75S transcripts.

A;Reference number: A91023

A;Accession: B24677

A;Molecule type: mRNA

A;Residues: 1-35 <GAL>

A;Note: the authors translated the codon TTA for residue 14 as Phe

C;Superfamily: unassigned Balbiani ring proteins

C;Keywords: tandem repeat

Query Match 11.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MRRV 21
|||
Db 9 MRRV 12

RESULT 23

D82125

hypothetical protein VC2034 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: D82125

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82125

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <HEI>

A;Cross-references: GB:AE004278; GB:AE003852; NID:g9656579; PIDN:AAF95182.1; GSPDB:GN00126; TIGR:VC2034

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC2034

A;Map position: 1

Query Match	11.8%;	Score 4;	DB 2;	Length 35;
Best Local Similarity	100.0%;	Pred. No. 1.2e+03;		
Matches	4;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

Qy	26 KKLQ 29
Db	24 KKLQ 27

RESULT 24

F95057

hypothetical protein SP0497 [imported] - *Streptococcus pneumoniae* (strain TIGR4)

C;Species: *Streptococcus pneumoniae*

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: F95057

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: F95057
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-36 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK74655.1; PID:g14971969; GSPDB:GN00164;
TIGR:SP4SP0497
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0497

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 10 KKLQ 13

RESULT 25

A84774

hypothetical protein At2g35870 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84774

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;
Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell,
C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin,
L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams,
M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver,
G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser,
C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: A84774

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <STO>

A;Cross-references: GB:AE002093; NID:g4510382; PIDN:AAD21470.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g35870

A;Map position: 2

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 4 KKLQ 7

RESULT 26

D47099

hypothetical protein (nac 3' region) - Klebsiella pneumoniae (fragment)

C;Species: *Klebsiella pneumoniae*
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 29-Sep-1999
C;Accession: D47099
R;Schwacha, A.; Bender, R.A.
J. Bacteriol. 175, 2107-2115, 1993
A;Title: The nac (nitrogen assimilation control) gene from *Klebsiella aerogenes*.
A;Reference number: A47099; MUID:93209957; PMID:8458853
A;Accession: D47099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-37 <SCH>
A;Cross-references: GB:L01114; NID:g149241; PIDN:AAA18175.1; PID:g149245
A;Experimental source: strain W70; isolate KC1043
C;Superfamily: conserved hypothetical protein b0819

Query Match 11.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MRRV 21
|||
Db 3 MRRV 6

RESULT 27

T12635

homeotic protein HAHB-2 - common sunflower (fragment)

C;Species: *Helianthus annuus* (common sunflower)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C;Accession: T12635
R;Chan, R.L.; Gonzalez, D.H.
Plant Physiol. 106, 1687-1688, 1994
A;Title: A cDNA encoding an HD-zip protein from sunflower.
A;Reference number: Z17563; MUID:95148747; PMID:7846169
A;Accession: T12635
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-37 <CHA>
A;Cross-references: EMBL:L22849; NID:g349258; PIDN:AAA63766.1; PID:g349259
C;Keywords: DNA binding; homeobox; transcription regulation

Query Match 11.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28
|||
Db 6 RKKL 9

RESULT 28

CKFHCS

sarcotoxin IC - flesh fly (*Sarcophaga peregrina*)

C;Species: *Sarcophaga peregrina*
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-1995
C;Accession: C22625
R;Okada, M.; Natori, S.

J. Biol. Chem. 260, 7174-7177, 1985

A;Title: Primary structure of sarcotoxin I, an antibacterial protein induced in the hemolymph of *Sarcophaga peregrina* (flesh fly) larvae.

A;Reference number: A92536; MUID:85207747; PMID:3888997

A;Accession: C22625

A;Molecule type: protein

A;Residues: 1-39 <OKA>

C;Comment: Sarcotoxins, which are potent bactericidal proteins, are produced in response to injury. They are cytotoxic to both Gram positive and Gram negative bacteria.

C;Superfamily: cecropin

C;Keywords: amidated carboxyl end; antibacterial; hemolymph

F;39/Modified site: amidated carboxyl end (Arg) #status predicted

Query Match 11.8%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
|||
Db 2 WLRK 5

RESULT 29

S77164

ycf32 protein - *Synechocystis* sp. (strain PCC 6803)

N;Alternate names: protein sml0007

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Accession: S77164

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S77164

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-39 <KAN>

A;Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAA17722.1; PID:g1652803

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Genetics:

A;Gene: ycf32

C;Superfamily: hypothetical protein ycf32

Query Match 11.8%; Score 4; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQDV 31

Db ||||
 31 LQDV 34

RESULT 30

S52343

hypothetical protein - *Lactococcus lactis* (fragment)

C;Species: *Lactococcus lactis*

C;Date: 08-May-1995 #sequence_revision 30-Jan-1998 #text_change 11-Jun-1999

C;Accession: S52343

R;Waterfield, N.R.; LePage, R.W.; Wilson, P.W.; Wells, J.M.

submitted to the EMBL Data Library, February 1995

A;Description: The isolation of lactococcal promoters and their use to investigate bacterial luciferase expression in *Lactococcus lactis*.

A;Reference number: S52330

A;Accession: S52343

A;Molecule type: DNA

A;Residues: 1-40 <WAT>

A;Cross-references: EMBL:Z48201; NID:g666059; PIDN:CAA88237.1; PID:g666060

A;Experimental source: sub species cremoris; strain MG1363

C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 11.8%; Score 4; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 RRVE 22

 ||||
Db 33 RRVE 36

RESULT 31

LFEC

leu operon leader peptide - *Escherichia coli* (strain K-12)

C;Species: *Escherichia coli*

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 01-Mar-2002

C;Accession: A30376; C64729; I56372; Q00032

R;Wessler, S.R.; Calvo, J.M.

J. Mol. Biol. 149, 579-597, 1981

A;Title: Control of leu operon expression in *Escherichia coli* by a transcription attenuation mechanism.

A;Reference number: A30376; MUID:82078077; PMID:6171647

A;Accession: A30376

A;Molecule type: DNA

A;Residues: 1-28 <WES>

A;Cross-references: GB:J01642; NID:g146601; PIDN:AAA24065.1; PID:g146602

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;

Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of *Escherichia coli* K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: C64729

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-28 <BLAT>

A;Cross-references: GB:AE000118; GB:U00096; NID:g1786262; PIDN:AAC73186.1;
PID:g1786263; UWGP:b0075

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: leuL; leuLP

A;Map position: 2 min

C;Function:

A;Description: involved in control of leucine operon transcription by
attenuation

C;Superfamily: leu leader peptide

Query Match 8.8%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 RRV 21
|||
Db 21 RRV 23

RESULT 32

A42272

brain-type creatine kinase, peptide B - spiny dogfish (fragment)

C;Species: Squalus acanthias (spiny dogfish)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997

C;Accession: A42272

R;Friedman, D.L.; Roberts, R.

J. Biol. Chem. 267, 4270-4276, 1992

A;Title: Purification and localization of brain-type creatine kinase in sodium
chloride transporting epithelia of the spiny dogfish, Squalus acanthias.

A;Reference number: A42272; MUID:92156175; PMID:1310991

A;Accession: A42272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <FRI>

A;Note: sequence extracted from NCBI backbone (NCBIP:82919)

C;Superfamily: creatine kinase; creatine kinase repeat homology

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 10 KKL 12

RESULT 33

C32416

phospholipase A2 (EC 3.1.1.4) pseudexin chain C - red-bellied black snake
(fragment)

C;Species: Pseudechis porphyriacus (red-bellied black snake)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 23-Jun-1993

C;Accession: C32416

R;Schmidt, J.J.; Middlebrook, J.L.

Toxicon 27, 805-818, 1989

A;Title: Purification, sequencing and characterization of pseudexin phospholipases A-2 from Pseudechis porphyriacus (Australian red-bellied black snake).

A;Reference number: A32416; MUID:89388835; PMID:2675391

A;Accession: C32416

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <SCH>

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7
|||
Db 3 IQL 5

RESULT 34

B60071

vasoactive intestinal peptide - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 20-Mar-1998

C;Accession: B60071

R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.

Regul. Pept. 32, 39-45, 1991

A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.

A;Reference number: A60071; MUID:91164506; PMID:2003150

A;Accession: B60071

A;Status: protein sequence not shown

A;Molecule type: protein

A;Residues: 1-28 <YUA>

A;Note: the sequence is identical with the human sequence

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 35

A60304

vasoactive intestinal peptide - dog

N;Alternate names: VIP

C;Species: Canis lupus familiaris (dog)

C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 20-Mar-1998

C;Accession: A60304

R;Eng, J.; Pan, Y.C.E.; Raufman, J.P.; Yalow, R.S.

Regul. Pept. Suppl. 3, S14, 1985

A;Title: Purification and sequencing of dog and guinea pig VIP's.
A;Reference number: A60304
A;Accession: A60304
A;Molecule type: protein
A;Residues: 1-28 <ENG>
C;Superfamily: glucagon
C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
|||
Db 23 LNS 25

RESULT 36

PN0047

signal transduction protein QM0017 - mouse (fragments)

C;Species: Mus musculus (house mouse)

C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 15-Oct-1999

C;Accession: PN0047

R;Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells.

A;Reference number: PN0041

A;Accession: PN0047

A;Molecule type: protein

A;Residues: 1-28 <KAT>

A;Experimental source: neuroblastoma cell

C;Comment: The molecular mass is 25,600 and the pI is 6.07. The amino-terminus is blocked.

C;Superfamily: signal transduction protein DJ-1

C;Keywords: brain

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NLG 12
|||
Db 14 NLG 16

RESULT 37

G90638

leu operon leader peptide [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 0509952)

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

C;Accession: G90638

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Ohtsubo, E.; Nakayama, K.; Murata, T.; Tanaka, M.; Tobe, T.; Iida, T.; Takami, H.; Honda, T.; Sasakawa, C.; Ogasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic comparison with a laboratory strain K-12.

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: G90638

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <HAY>

A;Cross-references: GB:BA000007; PIDN:BAB33502.1; PID:g13359535; GSPDB:GN00154

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs0079

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 RRV 21
|||
Db 21 RRV 23

RESULT 38

S56121

type I DNA methyltransferase M.EcoR124I chain HsdS - *Escherichia coli*
(fragments)

C;Species: *Escherichia coli*

C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995

C;Accession: S56121

R;Webb, M.; Taylor, I.A.; Firman, K.; Kneale, G.G.

J. Mol. Biol. 250, 181-190, 1995

A;Title: Probing the domain structure of the type IC DNA methyltransferase M.EcoR124I by limited proteolysis.

A;Reference number: S56121; MUID:95333175; PMID:7608969

A;Accession: S56121

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <WEB>

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 DVH 32
|||
Db 8 DVH 10

RESULT 39

S70894

hypothetical protein 1 - *Vibrio anguillarum* (fragment)

C;Species: *Vibrio anguillarum*

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C;Accession: S70894

R;O'Toole, R.; Milton, D.L.; Wolf-Watz, H.

Mol. Microbiol. 19, 625-637, 1996

A;Title: Chemotactic motility is required for invasion of the host by the fish pathogen *Vibrio anguillarum*.

A;Reference number: S70894; MUID:96228710; PMID:8830252

A;Accession: S70894

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <OTO>

A;Cross-references: GB:U36378; EMBL:L47344; NID:g1020321; PIDN:AAB38488.1;

PID:g1723992

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 18 LNS 20

RESULT 40

S22469

hypothetical protein 1 - *Prochlorothrix hollandica*

C;Species: *Prochlorothrix hollandica*

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Oct-1999

C;Accession: S22469; S16850

R;Greer, K.L.; Golden, S.S.

Plant Mol. Biol. 19, 355-365, 1992

A;Title: Conserved relationship between psbH and petBD genes: presence of a shared upstream element in *Prochlorothrix hollandica*.

A;Reference number: S22469; MUID:92322967; PMID:1623188

A;Accession: S22469

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <GRE>

A;Cross-references: EMBL:X60313; NID:g45528; PIDN:CAA42858.1; PID:g45529

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVS 3
|||
Db 4 SVS 6

Search completed: January 14, 2004, 10:37:24

Job time : 11.0623 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:37:44 ; Search time 22.8785 Seconds
(without alignments)
303.882 Million cell updates/sec

Title: US-09-843-221A-164
Perfect score: 34
Sequence: 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 762491 seqs, 204481190 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28045

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%				Description
Result	Query					
No.	Score	Match	Length	DB	ID	

1	34	100.0	34	11	US-09-843-221A-19	Sequence 19, Appl
2	34	100.0	34	11	US-09-843-221A-164	Sequence 164, App
3	30	88.2	30	11	US-09-843-221A-42	Sequence 42, Appl
4	18	52.9	28	11	US-09-843-221A-52	Sequence 52, Appl
5	18	52.9	28	11	US-09-843-221A-168	Sequence 168, App
6	18	52.9	29	11	US-09-843-221A-51	Sequence 51, Appl
7	18	52.9	29	11	US-09-843-221A-167	Sequence 167, App
8	18	52.9	30	11	US-09-843-221A-39	Sequence 39, Appl
9	18	52.9	30	11	US-09-843-221A-50	Sequence 50, Appl
10	18	52.9	30	11	US-09-843-221A-124	Sequence 124, App
11	18	52.9	30	11	US-09-843-221A-125	Sequence 125, App
12	18	52.9	30	11	US-09-843-221A-126	Sequence 126, App
13	18	52.9	30	11	US-09-843-221A-127	Sequence 127, App
14	18	52.9	30	11	US-09-843-221A-166	Sequence 166, App
15	18	52.9	31	9	US-09-169-786-2	Sequence 2, Appli
16	18	52.9	31	11	US-09-843-221A-27	Sequence 27, Appl
17	18	52.9	31	11	US-09-843-221A-28	Sequence 28, Appl
18	18	52.9	31	11	US-09-843-221A-165	Sequence 165, App
19	18	52.9	31	12	US-10-031-874A-206	Sequence 206, App
20	18	52.9	33	12	US-10-361-928-9	Sequence 9, Appli
21	18	52.9	34	9	US-09-169-786-3	Sequence 3, Appli
22	18	52.9	34	10	US-09-928-047B-6	Sequence 6, Appli
23	18	52.9	34	11	US-09-843-221A-16	Sequence 16, Appl
24	18	52.9	34	11	US-09-843-221A-88	Sequence 88, Appl
25	18	52.9	34	11	US-09-843-221A-89	Sequence 89, Appl
26	18	52.9	34	11	US-09-843-221A-90	Sequence 90, Appl
27	18	52.9	34	11	US-09-843-221A-91	Sequence 91, Appl
28	18	52.9	34	11	US-09-843-221A-92	Sequence 92, Appl
29	18	52.9	34	11	US-09-843-221A-128	Sequence 128, App
30	18	52.9	34	11	US-09-843-221A-161	Sequence 161, App
31	18	52.9	34	12	US-09-928-048A-6	Sequence 6, Appli
32	18	52.9	34	12	US-10-361-928-8	Sequence 8, Appli
33	18	52.9	34	12	US-10-340-484-15	Sequence 15, Appl
34	18	52.9	34	12	US-10-340-484-16	Sequence 16, Appl
35	18	52.9	34	14	US-10-016-403-5	Sequence 5, Appli
36	18	52.9	34	14	US-10-016-403-7	Sequence 7, Appli
37	18	52.9	34	14	US-10-097-079-1	Sequence 1, Appli
38	18	52.9	37	12	US-10-168-185-9	Sequence 9, Appli
39	18	52.9	38	9	US-09-169-786-4	Sequence 4, Appli
40	18	52.9	38	11	US-09-843-221A-14	Sequence 14, Appl
41	18	52.9	38	12	US-10-245-707-1	Sequence 1, Appli
42	17	50.0	30	11	US-09-843-221A-43	Sequence 43, Appl
43	17	50.0	33	12	US-10-361-928-3	Sequence 3, Appli
44	17	50.0	33	12	US-10-361-928-6	Sequence 6, Appli
45	17	50.0	34	11	US-09-843-221A-20	Sequence 20, Appl
46	17	50.0	34	12	US-10-361-928-1	Sequence 1, Appli
47	17	50.0	34	12	US-10-361-928-2	Sequence 2, Appli
48	17	50.0	34	12	US-10-361-928-5	Sequence 5, Appli
49	17	50.0	34	12	US-10-340-484-17	Sequence 17, Appl
50	17	50.0	37	11	US-09-843-221A-15	Sequence 15, Appl
51	15	44.1	28	11	US-09-843-221A-32	Sequence 32, Appl
52	15	44.1	28	11	US-09-843-221A-34	Sequence 34, Appl
53	15	44.1	30	11	US-09-843-221A-47	Sequence 47, Appl
54	15	44.1	32	11	US-09-843-221A-30	Sequence 30, Appl
55	15	44.1	34	11	US-09-843-221A-17	Sequence 17, Appl
56	15	44.1	34	11	US-09-843-221A-18	Sequence 18, Appl

57	15	44.1	34	11	US-09-843-221A-22	Sequence 22, Appl
58	15	44.1	34	11	US-09-843-221A-24	Sequence 24, Appl
59	15	44.1	34	11	US-09-843-221A-162	Sequence 162, App
60	15	44.1	34	11	US-09-843-221A-163	Sequence 163, App
61	15	44.1	34	12	US-10-372-095-24	Sequence 24, Appl
62	15	44.1	34	12	US-10-340-484-18	Sequence 18, Appl
63	15	44.1	34	12	US-10-340-484-19	Sequence 19, Appl
64	15	44.1	34	12	US-10-340-484-20	Sequence 20, Appl
65	15	44.1	34	14	US-10-016-403-6	Sequence 6, Appli
66	15	44.1	40	15	US-10-014-162-111	Sequence 111, App
67	14	41.2	28	11	US-09-843-221A-33	Sequence 33, Appl
68	14	41.2	28	11	US-09-843-221A-35	Sequence 35, Appl
69	14	41.2	28	11	US-09-843-221A-36	Sequence 36, Appl
70	14	41.2	30	11	US-09-843-221A-48	Sequence 48, Appl
71	14	41.2	32	11	US-09-843-221A-29	Sequence 29, Appl
72	14	41.2	32	11	US-09-843-221A-31	Sequence 31, Appl
73	14	41.2	34	11	US-09-843-221A-21	Sequence 21, Appl
74	14	41.2	34	11	US-09-843-221A-23	Sequence 23, Appl
75	14	41.2	34	11	US-09-843-221A-25	Sequence 25, Appl
76	14	41.2	34	12	US-10-340-484-22	Sequence 22, Appl
77	14	41.2	34	12	US-10-340-484-23	Sequence 23, Appl
78	13	38.2	34	9	US-09-169-786-11	Sequence 11, Appl
79	12	35.3	28	11	US-09-843-221A-93	Sequence 93, Appl
80	12	35.3	28	11	US-09-843-221A-94	Sequence 94, Appl
81	12	35.3	28	11	US-09-843-221A-95	Sequence 95, Appl
82	12	35.3	28	11	US-09-843-221A-96	Sequence 96, Appl
83	12	35.3	28	11	US-09-843-221A-97	Sequence 97, Appl
84	11	32.4	28	11	US-09-843-221A-53	Sequence 53, Appl
85	11	32.4	28	11	US-09-843-221A-54	Sequence 54, Appl
86	11	32.4	28	11	US-09-843-221A-55	Sequence 55, Appl
87	11	32.4	30	11	US-09-843-221A-40	Sequence 40, Appl
88	11	32.4	30	11	US-09-843-221A-41	Sequence 41, Appl
89	11	32.4	30	11	US-09-843-221A-44	Sequence 44, Appl
90	11	32.4	30	11	US-09-843-221A-45	Sequence 45, Appl
91	11	32.4	30	11	US-09-843-221A-46	Sequence 46, Appl
92	11	32.4	34	11	US-09-843-221A-26	Sequence 26, Appl
93	11	32.4	34	12	US-10-372-095-22	Sequence 22, Appl
94	9	26.5	28	14	US-10-097-079-54	Sequence 54, Appl
95	9	26.5	28	14	US-10-097-079-62	Sequence 62, Appl
96	9	26.5	28	14	US-10-097-079-65	Sequence 65, Appl
97	9	26.5	28	14	US-10-097-079-79	Sequence 79, Appl
98	9	26.5	29	14	US-10-097-079-53	Sequence 53, Appl
99	9	26.5	29	14	US-10-097-079-63	Sequence 63, Appl
100	9	26.5	30	14	US-10-097-079-52	Sequence 52, Appl
101	9	26.5	30	14	US-10-097-079-64	Sequence 64, Appl
102	9	26.5	31	14	US-10-097-079-3	Sequence 3, Appli
103	9	26.5	31	14	US-10-097-079-4	Sequence 4, Appli
104	9	26.5	31	14	US-10-097-079-5	Sequence 5, Appli
105	9	26.5	31	14	US-10-097-079-6	Sequence 6, Appli
106	9	26.5	31	14	US-10-097-079-7	Sequence 7, Appli
107	9	26.5	31	14	US-10-097-079-8	Sequence 8, Appli
108	9	26.5	31	14	US-10-097-079-9	Sequence 9, Appli
109	9	26.5	31	14	US-10-097-079-10	Sequence 10, Appl
110	9	26.5	31	14	US-10-097-079-20	Sequence 20, Appl
111	9	26.5	31	14	US-10-097-079-21	Sequence 21, Appl
112	9	26.5	31	14	US-10-097-079-22	Sequence 22, Appl
113	9	26.5	31	14	US-10-097-079-23	Sequence 23, Appl

114	9	26.5	31	14	US-10-097-079-24	Sequence 24, Appl
115	9	26.5	31	14	US-10-097-079-25	Sequence 25, Appl
116	9	26.5	31	14	US-10-097-079-26	Sequence 26, Appl
117	9	26.5	31	14	US-10-097-079-27	Sequence 27, Appl
118	9	26.5	31	14	US-10-097-079-36	Sequence 36, Appl
119	9	26.5	31	14	US-10-097-079-37	Sequence 37, Appl
120	9	26.5	31	14	US-10-097-079-38	Sequence 38, Appl
121	9	26.5	31	14	US-10-097-079-39	Sequence 39, Appl
122	9	26.5	31	14	US-10-097-079-47	Sequence 47, Appl
123	9	26.5	31	14	US-10-097-079-48	Sequence 48, Appl
124	9	26.5	31	14	US-10-097-079-49	Sequence 49, Appl
125	9	26.5	31	14	US-10-097-079-50	Sequence 50, Appl
126	9	26.5	31	14	US-10-097-079-51	Sequence 51, Appl
127	9	26.5	31	14	US-10-097-079-69	Sequence 69, Appl
128	9	26.5	31	14	US-10-097-079-70	Sequence 70, Appl
129	9	26.5	31	14	US-10-097-079-74	Sequence 74, Appl
130	9	26.5	31	14	US-10-097-079-81	Sequence 81, Appl
131	9	26.5	31	14	US-10-097-079-82	Sequence 82, Appl
132	9	26.5	31	14	US-10-097-079-83	Sequence 83, Appl
133	9	26.5	31	14	US-10-097-079-84	Sequence 84, Appl
134	9	26.5	31	14	US-10-097-079-85	Sequence 85, Appl
135	9	26.5	34	14	US-10-097-079-46	Sequence 46, Appl
136	8	23.5	28	14	US-10-097-079-78	Sequence 78, Appl
137	8	23.5	30	11	US-09-843-221A-49	Sequence 49, Appl
138	8	23.5	30	11	US-09-843-221A-158	Sequence 158, App
139	8	23.5	30	11	US-09-843-221A-159	Sequence 159, App
140	8	23.5	31	9	US-09-169-786-9	Sequence 9, Appli
141	8	23.5	31	9	US-09-169-786-10	Sequence 10, Appl
142	8	23.5	31	14	US-10-097-079-11	Sequence 11, Appl
143	8	23.5	31	14	US-10-097-079-19	Sequence 19, Appl
144	8	23.5	31	14	US-10-097-079-28	Sequence 28, Appl
145	8	23.5	31	14	US-10-097-079-35	Sequence 35, Appl
146	8	23.5	31	14	US-10-097-079-40	Sequence 40, Appl
147	8	23.5	31	14	US-10-097-079-45	Sequence 45, Appl
148	8	23.5	31	14	US-10-097-079-68	Sequence 68, Appl
149	8	23.5	31	14	US-10-097-079-73	Sequence 73, Appl
150	8	23.5	31	14	US-10-097-079-76	Sequence 76, Appl
151	8	23.5	31	14	US-10-097-079-80	Sequence 80, Appl
152	8	23.5	34	11	US-09-843-221A-122	Sequence 122, App
153	8	23.5	34	11	US-09-843-221A-123	Sequence 123, App
154	8	23.5	34	14	US-10-097-079-75	Sequence 75, Appl
155	7	20.6	31	14	US-10-097-079-12	Sequence 12, Appl
156	7	20.6	31	14	US-10-097-079-18	Sequence 18, Appl
157	7	20.6	31	14	US-10-097-079-29	Sequence 29, Appl
158	7	20.6	31	14	US-10-097-079-34	Sequence 34, Appl
159	7	20.6	31	14	US-10-097-079-41	Sequence 41, Appl
160	7	20.6	31	14	US-10-097-079-44	Sequence 44, Appl
161	7	20.6	31	14	US-10-097-079-66	Sequence 66, Appl
162	7	20.6	31	14	US-10-097-079-67	Sequence 67, Appl
163	7	20.6	34	12	US-10-340-484-24	Sequence 24, Appl
164	6	17.6	30	11	US-09-843-221A-77	Sequence 77, Appl
165	6	17.6	31	14	US-10-097-079-13	Sequence 13, Appl
166	6	17.6	31	14	US-10-097-079-14	Sequence 14, Appl
167	6	17.6	31	14	US-10-097-079-15	Sequence 15, Appl
168	6	17.6	31	14	US-10-097-079-16	Sequence 16, Appl
169	6	17.6	31	14	US-10-097-079-17	Sequence 17, Appl
170	6	17.6	31	14	US-10-097-079-30	Sequence 30, Appl

171	6	17.6	31	14	US-10-097-079-31	Sequence 31, Appl
172	6	17.6	31	14	US-10-097-079-32	Sequence 32, Appl
173	6	17.6	31	14	US-10-097-079-33	Sequence 33, Appl
174	6	17.6	31	14	US-10-097-079-42	Sequence 42, Appl
175	6	17.6	31	14	US-10-097-079-43	Sequence 43, Appl
176	6	17.6	31	14	US-10-097-079-86	Sequence 86, Appl
177	6	17.6	31	14	US-10-097-079-87	Sequence 87, Appl
178	6	17.6	31	14	US-10-097-079-88	Sequence 88, Appl
179	6	17.6	36	11	US-09-843-221A-65	Sequence 65, Appl
180	5	14.7	28	11	US-09-843-221A-69	Sequence 69, Appl
181	5	14.7	28	11	US-09-843-221A-169	Sequence 169, App
182	5	14.7	34	9	US-09-864-761-38558	Sequence 38558, A
183	5	14.7	34	12	US-10-317-832-178	Sequence 178, App
184	5	14.7	38	9	US-09-864-761-49110	Sequence 49110, A
185	4	11.8	28	9	US-09-864-761-37690	Sequence 37690, A
186	4	11.8	28	9	US-09-864-761-47465	Sequence 47465, A
187	4	11.8	28	9	US-09-864-761-47891	Sequence 47891, A
188	4	11.8	28	9	US-09-929-818-122	Sequence 122, App
189	4	11.8	28	9	US-09-929-818-200	Sequence 200, App
190	4	11.8	28	10	US-09-003-869-153	Sequence 153, App
191	4	11.8	28	10	US-09-999-745-38	Sequence 38, Appl
192	4	11.8	28	10	US-09-554-000-22	Sequence 22, Appl
193	4	11.8	28	11	US-09-756-690A-153	Sequence 153, App
194	4	11.8	28	11	US-09-776-724A-198	Sequence 198, App
195	4	11.8	28	12	US-10-029-386-28289	Sequence 28289, A
196	4	11.8	28	15	US-10-157-224A-153	Sequence 153, App
197	4	11.8	28	15	US-10-187-051-153	Sequence 153, App
198	4	11.8	29	9	US-09-730-379B-5	Sequence 5, Appli
199	4	11.8	29	11	US-09-983-802-386	Sequence 386, App
200	4	11.8	29	11	US-09-983-802-480	Sequence 480, App
201	4	11.8	29	11	US-09-969-730-133	Sequence 133, App
202	4	11.8	29	11	US-09-095-478-24	Sequence 24, Appl
203	4	11.8	29	12	US-09-933-767-1006	Sequence 1006, Ap
204	4	11.8	29	15	US-10-023-282-1006	Sequence 1006, Ap
205	4	11.8	29	15	US-10-106-698-5404	Sequence 5404, Ap
206	4	11.8	29	15	US-10-197-954-111	Sequence 111, App
207	4	11.8	30	9	US-09-864-761-41441	Sequence 41441, A
208	4	11.8	30	9	US-09-864-761-46868	Sequence 46868, A
209	4	11.8	30	10	US-09-756-983-20	Sequence 20, Appl
210	4	11.8	30	11	US-09-774-639-191	Sequence 191, App
211	4	11.8	30	12	US-09-911-261A-20	Sequence 20, Appl
212	4	11.8	30	12	US-10-310-113-19	Sequence 19, Appl
213	4	11.8	30	12	US-09-933-767-821	Sequence 821, App
214	4	11.8	30	12	US-10-173-551-40	Sequence 40, Appl
215	4	11.8	30	15	US-10-188-947-11	Sequence 11, Appl
216	4	11.8	30	15	US-10-057-408-20	Sequence 20, Appl
217	4	11.8	30	15	US-10-023-282-821	Sequence 821, App
218	4	11.8	30	15	US-10-267-209-3	Sequence 3, Appli
219	4	11.8	31	9	US-09-864-761-38725	Sequence 38725, A
220	4	11.8	31	9	US-09-864-761-40464	Sequence 40464, A
221	4	11.8	31	9	US-09-864-761-44182	Sequence 44182, A
222	4	11.8	31	10	US-09-738-626-6281	Sequence 6281, Ap
223	4	11.8	31	12	US-10-360-053-20	Sequence 20, Appl
224	4	11.8	31	12	US-09-933-767-1001	Sequence 1001, Ap
225	4	11.8	31	12	US-10-029-386-32285	Sequence 32285, A
226	4	11.8	31	12	US-10-264-049-3767	Sequence 3767, Ap
227	4	11.8	31	15	US-10-023-282-1001	Sequence 1001, Ap

228	4	11.8	31	15	US-10-106-698-7956	Sequence 7956, Ap
229	4	11.8	32	9	US-09-864-761-48632	Sequence 48632, A
230	4	11.8	32	9	US-09-281-717-16	Sequence 16, Appl
231	4	11.8	32	11	US-09-809-391-442	Sequence 442, App
232	4	11.8	32	12	US-09-882-171-442	Sequence 442, App
233	4	11.8	32	12	US-10-310-113-23	Sequence 23, Appl
234	4	11.8	32	12	US-10-310-113-134	Sequence 134, App
235	4	11.8	32	12	US-10-310-113-135	Sequence 135, App
236	4	11.8	32	12	US-10-310-113-136	Sequence 136, App
237	4	11.8	32	12	US-10-164-279-39	Sequence 39, Appl
238	4	11.8	32	12	US-10-164-279-43	Sequence 43, Appl
239	4	11.8	33	9	US-09-864-761-35714	Sequence 35714, A
240	4	11.8	33	9	US-09-864-761-38816	Sequence 38816, A
241	4	11.8	33	9	US-09-864-761-48253	Sequence 48253, A
242	4	11.8	33	9	US-09-864-761-49019	Sequence 49019, A
243	4	11.8	33	9	US-09-925-299-1526	Sequence 1526, Ap
244	4	11.8	33	10	US-09-911-969-16	Sequence 16, Appl
245	4	11.8	33	11	US-09-925-299-1526	Sequence 1526, Ap
246	4	11.8	33	11	US-09-809-391-660	Sequence 660, App
247	4	11.8	33	12	US-09-882-171-660	Sequence 660, App
248	4	11.8	33	12	US-09-933-767-368	Sequence 368, App
249	4	11.8	33	12	US-10-164-279-63	Sequence 63, Appl
250	4	11.8	33	14	US-10-215-297-4	Sequence 4, Appli
251	4	11.8	33	15	US-10-215-298-4	Sequence 4, Appli
252	4	11.8	33	15	US-10-081-816-110	Sequence 110, App
253	4	11.8	33	15	US-10-023-282-368	Sequence 368, App
254	4	11.8	34	9	US-09-864-761-44185	Sequence 44185, A
255	4	11.8	34	9	US-09-864-761-44916	Sequence 44916, A
256	4	11.8	34	9	US-09-864-761-45430	Sequence 45430, A
257	4	11.8	34	9	US-09-864-761-48511	Sequence 48511, A
258	4	11.8	34	12	US-10-231-417-538	Sequence 538, App
259	4	11.8	34	12	US-10-029-386-27795	Sequence 27795, A
260	4	11.8	34	15	US-10-106-698-8037	Sequence 8037, Ap
261	4	11.8	35	9	US-09-925-299-1258	Sequence 1258, Ap
262	4	11.8	35	10	US-09-811-824-7	Sequence 7, Appli
263	4	11.8	35	11	US-09-983-802-486	Sequence 486, App
264	4	11.8	35	11	US-09-820-843A-106	Sequence 106, App
265	4	11.8	35	11	US-09-925-299-1258	Sequence 1258, Ap
266	4	11.8	35	12	US-10-289-660-75	Sequence 75, Appl
267	4	11.8	35	12	US-10-340-484-13	Sequence 13, Appl
268	4	11.8	35	12	US-10-012-952A-147	Sequence 147, App
269	4	11.8	35	12	US-10-062-599-138	Sequence 138, App
270	4	11.8	35	12	US-10-345-072-165	Sequence 165, App
271	4	11.8	35	15	US-10-133-128-75	Sequence 75, Appl
272	4	11.8	35	15	US-10-062-831-138	Sequence 138, App
273	4	11.8	36	8	US-08-851-965-24	Sequence 24, Appl
274	4	11.8	36	9	US-09-864-761-34257	Sequence 34257, A
275	4	11.8	36	9	US-09-864-761-39771	Sequence 39771, A
276	4	11.8	36	9	US-09-864-761-46707	Sequence 46707, A
277	4	11.8	36	9	US-09-864-761-48628	Sequence 48628, A
278	4	11.8	36	10	US-09-454-533-30	Sequence 30, Appl
279	4	11.8	36	12	US-10-340-484-12	Sequence 12, Appl
280	4	11.8	36	12	US-09-962-756-1266	Sequence 1266, Ap
281	4	11.8	36	12	US-10-029-386-27817	Sequence 27817, A
282	4	11.8	36	12	US-10-253-471-1266	Sequence 1266, Ap
283	4	11.8	36	14	US-10-002-344A-205	Sequence 205, App
284	4	11.8	36	15	US-10-050-704-192	Sequence 192, App

285	4	11.8	37	8	US-08-851-965-22	Sequence 22, Appl
286	4	11.8	37	8	US-08-851-965-23	Sequence 23, Appl
287	4	11.8	37	8	US-08-851-965-25	Sequence 25, Appl
288	4	11.8	37	8	US-08-851-965-26	Sequence 26, Appl
289	4	11.8	37	8	US-08-851-965-27	Sequence 27, Appl
290	4	11.8	37	9	US-09-758-318-16	Sequence 16, Appl
291	4	11.8	37	9	US-09-864-761-38287	Sequence 38287, A
292	4	11.8	37	9	US-09-864-761-41884	Sequence 41884, A
293	4	11.8	37	9	US-09-864-761-42087	Sequence 42087, A
294	4	11.8	37	10	US-09-908-805B-79	Sequence 79, Appl
295	4	11.8	37	10	US-09-454-533-6	Sequence 6, Appli
296	4	11.8	37	10	US-09-454-533-28	Sequence 28, Appl
297	4	11.8	37	10	US-09-454-533-29	Sequence 29, Appl
298	4	11.8	37	10	US-09-454-533-31	Sequence 31, Appl
299	4	11.8	37	10	US-09-454-533-32	Sequence 32, Appl
300	4	11.8	37	10	US-09-454-533-33	Sequence 33, Appl
301	4	11.8	37	11	US-09-764-872-347	Sequence 347, App
302	4	11.8	37	12	US-10-340-783-16	Sequence 16, Appl
303	4	11.8	37	12	US-10-012-952A-209	Sequence 209, App
304	4	11.8	37	12	US-10-339-740-265	Sequence 265, App
305	4	11.8	37	12	US-10-283-403-9	Sequence 9, Appli
306	4	11.8	37	12	US-10-370-570-10	Sequence 10, Appl
307	4	11.8	37	15	US-10-082-830-161	Sequence 161, App
308	4	11.8	37	15	US-10-106-698-6085	Sequence 6085, Ap
309	4	11.8	38	9	US-09-250-883-21	Sequence 21, Appl
310	4	11.8	38	9	US-09-864-761-34617	Sequence 34617, A
311	4	11.8	38	9	US-09-864-761-38489	Sequence 38489, A
312	4	11.8	38	9	US-09-864-761-44123	Sequence 44123, A
313	4	11.8	38	9	US-09-864-761-44436	Sequence 44436, A
314	4	11.8	39	9	US-09-864-761-41089	Sequence 41089, A
315	4	11.8	39	9	US-09-864-761-41410	Sequence 41410, A
316	4	11.8	39	10	US-09-003-869-25	Sequence 25, Appl
317	4	11.8	39	11	US-09-983-802-384	Sequence 384, App
318	4	11.8	39	11	US-09-756-690A-25	Sequence 25, Appl
319	4	11.8	39	15	US-10-157-224A-25	Sequence 25, Appl
320	4	11.8	39	15	US-10-187-051-25	Sequence 25, Appl
321	4	11.8	39	15	US-10-106-698-7822	Sequence 7822, Ap
322	4	11.8	40	9	US-09-864-761-40979	Sequence 40979, A
323	4	11.8	40	11	US-09-764-891-2762	Sequence 2762, Ap
324	4	11.8	40	11	US-09-764-891-3795	Sequence 3795, Ap
325	4	11.8	40	12	US-10-326-040-24	Sequence 24, Appl
326	4	11.8	40	12	US-10-326-040-25	Sequence 25, Appl
327	4	11.8	40	12	US-10-058-053A-81	Sequence 81, Appl
328	4	11.8	40	12	US-10-058-053A-264	Sequence 264, App
329	4	11.8	40	15	US-10-091-572-223	Sequence 223, App
330	3	8.8	28	8	US-08-908-884-7	Sequence 7, Appli
331	3	8.8	28	9	US-09-799-983-16	Sequence 16, Appl
332	3	8.8	28	9	US-09-799-983-18	Sequence 18, Appl
333	3	8.8	28	9	US-09-765-527-30	Sequence 30, Appl
334	3	8.8	28	9	US-09-765-527-139	Sequence 139, App
335	3	8.8	28	9	US-09-765-527-140	Sequence 140, App
336	3	8.8	28	9	US-09-765-527-142	Sequence 142, App
337	3	8.8	28	9	US-09-765-527-143	Sequence 143, App
338	3	8.8	28	9	US-09-895-072-27	Sequence 27, Appl
339	3	8.8	28	9	US-09-864-761-33837	Sequence 33837, A
340	3	8.8	28	9	US-09-864-761-34933	Sequence 34933, A
341	3	8.8	28	9	US-09-864-761-34971	Sequence 34971, A

342	3	8.8	28	9	US-09-864-761-35640	Sequence 35640, A
343	3	8.8	28	9	US-09-864-761-35827	Sequence 35827, A
344	3	8.8	28	9	US-09-864-761-36728	Sequence 36728, A
345	3	8.8	28	9	US-09-864-761-37848	Sequence 37848, A
346	3	8.8	28	9	US-09-864-761-37919	Sequence 37919, A
347	3	8.8	28	9	US-09-864-761-37927	Sequence 37927, A
348	3	8.8	28	9	US-09-864-761-39493	Sequence 39493, A
349	3	8.8	28	9	US-09-864-761-39762	Sequence 39762, A
350	3	8.8	28	9	US-09-864-761-39984	Sequence 39984, A
351	3	8.8	28	9	US-09-864-761-40236	Sequence 40236, A
352	3	8.8	28	9	US-09-864-761-40300	Sequence 40300, A
353	3	8.8	28	9	US-09-864-761-41015	Sequence 41015, A
354	3	8.8	28	9	US-09-864-761-41850	Sequence 41850, A
355	3	8.8	28	9	US-09-864-761-42177	Sequence 42177, A
356	3	8.8	28	9	US-09-864-761-42253	Sequence 42253, A
357	3	8.8	28	9	US-09-864-761-43275	Sequence 43275, A
358	3	8.8	28	9	US-09-864-761-43290	Sequence 43290, A
359	3	8.8	28	9	US-09-864-761-43834	Sequence 43834, A
360	3	8.8	28	9	US-09-864-761-43979	Sequence 43979, A
361	3	8.8	28	9	US-09-864-761-44041	Sequence 44041, A
362	3	8.8	28	9	US-09-864-761-44733	Sequence 44733, A
363	3	8.8	28	9	US-09-864-761-45427	Sequence 45427, A
364	3	8.8	28	9	US-09-864-761-46128	Sequence 46128, A
365	3	8.8	28	9	US-09-864-761-46536	Sequence 46536, A
366	3	8.8	28	9	US-09-864-761-47128	Sequence 47128, A
367	3	8.8	28	9	US-09-864-761-47968	Sequence 47968, A
368	3	8.8	28	9	US-09-864-761-48171	Sequence 48171, A
369	3	8.8	28	9	US-09-864-761-48316	Sequence 48316, A
370	3	8.8	28	9	US-09-864-761-49082	Sequence 49082, A
371	3	8.8	28	9	US-09-962-055-26	Sequence 26, Appl
372	3	8.8	28	9	US-09-925-301-1524	Sequence 1524, Ap
373	3	8.8	28	9	US-09-925-299-1173	Sequence 1173, Ap
374	3	8.8	28	9	US-09-728-721-19	Sequence 19, Appl
375	3	8.8	28	9	US-09-728-721-23	Sequence 23, Appl
376	3	8.8	28	9	US-09-908-323-7	Sequence 7, Appli
377	3	8.8	28	9	US-09-881-490-5	Sequence 5, Appli
378	3	8.8	28	9	US-09-881-490-110	Sequence 110, App
379	3	8.8	28	9	US-09-881-490-111	Sequence 111, App
380	3	8.8	28	9	US-09-881-490-113	Sequence 113, App
381	3	8.8	28	9	US-09-881-490-114	Sequence 114, App
382	3	8.8	28	9	US-09-879-666-4	Sequence 4, Appli
383	3	8.8	28	9	US-09-929-818-1	Sequence 1, Appli
384	3	8.8	28	9	US-09-929-818-2	Sequence 2, Appli
385	3	8.8	28	9	US-09-929-818-3	Sequence 3, Appli
386	3	8.8	28	9	US-09-929-818-4	Sequence 4, Appli
387	3	8.8	28	9	US-09-929-818-5	Sequence 5, Appli
388	3	8.8	28	9	US-09-929-818-6	Sequence 6, Appli
389	3	8.8	28	9	US-09-929-818-7	Sequence 7, Appli
390	3	8.8	28	9	US-09-929-818-8	Sequence 8, Appli
391	3	8.8	28	9	US-09-929-818-9	Sequence 9, Appli
392	3	8.8	28	9	US-09-929-818-10	Sequence 10, Appl
393	3	8.8	28	9	US-09-929-818-11	Sequence 11, Appl
394	3	8.8	28	9	US-09-929-818-12	Sequence 12, Appl
395	3	8.8	28	9	US-09-929-818-13	Sequence 13, Appl
396	3	8.8	28	9	US-09-929-818-14	Sequence 14, Appl
397	3	8.8	28	9	US-09-929-818-15	Sequence 15, Appl
398	3	8.8	28	9	US-09-929-818-16	Sequence 16, Appl

399	3	8.8	28	9	US-09-929-818-17	Sequence 17, Appl
400	3	8.8	28	9	US-09-929-818-18	Sequence 18, Appl
401	3	8.8	28	9	US-09-929-818-19	Sequence 19, Appl
402	3	8.8	28	9	US-09-929-818-20	Sequence 20, Appl
403	3	8.8	28	9	US-09-929-818-21	Sequence 21, Appl
404	3	8.8	28	9	US-09-929-818-22	Sequence 22, Appl
405	3	8.8	28	9	US-09-929-818-23	Sequence 23, Appl
406	3	8.8	28	9	US-09-929-818-24	Sequence 24, Appl
407	3	8.8	28	9	US-09-929-818-25	Sequence 25, Appl
408	3	8.8	28	9	US-09-929-818-26	Sequence 26, Appl
409	3	8.8	28	9	US-09-929-818-27	Sequence 27, Appl
410	3	8.8	28	9	US-09-929-818-28	Sequence 28, Appl
411	3	8.8	28	9	US-09-929-818-29	Sequence 29, Appl
412	3	8.8	28	9	US-09-929-818-30	Sequence 30, Appl
413	3	8.8	28	9	US-09-929-818-31	Sequence 31, Appl
414	3	8.8	28	9	US-09-929-818-32	Sequence 32, Appl
415	3	8.8	28	9	US-09-929-818-33	Sequence 33, Appl
416	3	8.8	28	9	US-09-929-818-34	Sequence 34, Appl
417	3	8.8	28	9	US-09-929-818-35	Sequence 35, Appl
418	3	8.8	28	9	US-09-929-818-36	Sequence 36, Appl
419	3	8.8	28	9	US-09-929-818-37	Sequence 37, Appl
420	3	8.8	28	9	US-09-929-818-38	Sequence 38, Appl
421	3	8.8	28	9	US-09-929-818-39	Sequence 39, Appl
422	3	8.8	28	9	US-09-929-818-40	Sequence 40, Appl
423	3	8.8	28	9	US-09-929-818-41	Sequence 41, Appl
424	3	8.8	28	9	US-09-929-818-42	Sequence 42, Appl
425	3	8.8	28	9	US-09-929-818-43	Sequence 43, Appl
426	3	8.8	28	9	US-09-929-818-44	Sequence 44, Appl
427	3	8.8	28	9	US-09-929-818-45	Sequence 45, Appl
428	3	8.8	28	9	US-09-929-818-46	Sequence 46, Appl
429	3	8.8	28	9	US-09-929-818-47	Sequence 47, Appl
430	3	8.8	28	9	US-09-929-818-48	Sequence 48, Appl
431	3	8.8	28	9	US-09-929-818-49	Sequence 49, Appl
432	3	8.8	28	9	US-09-929-818-50	Sequence 50, Appl
433	3	8.8	28	9	US-09-929-818-51	Sequence 51, Appl
434	3	8.8	28	9	US-09-929-818-52	Sequence 52, Appl
435	3	8.8	28	9	US-09-929-818-53	Sequence 53, Appl
436	3	8.8	28	9	US-09-929-818-54	Sequence 54, Appl
437	3	8.8	28	9	US-09-929-818-61	Sequence 61, Appl
438	3	8.8	28	9	US-09-929-818-62	Sequence 62, Appl
439	3	8.8	28	9	US-09-929-818-66	Sequence 66, Appl
440	3	8.8	28	9	US-09-929-818-69	Sequence 69, Appl
441	3	8.8	28	9	US-09-929-818-76	Sequence 76, Appl
442	3	8.8	28	9	US-09-929-818-77	Sequence 77, Appl
443	3	8.8	28	9	US-09-929-818-80	Sequence 80, Appl
444	3	8.8	28	9	US-09-929-818-87	Sequence 87, Appl
445	3	8.8	28	9	US-09-929-818-94	Sequence 94, Appl
446	3	8.8	28	9	US-09-929-818-95	Sequence 95, Appl
447	3	8.8	28	9	US-09-929-818-97	Sequence 97, Appl
448	3	8.8	28	9	US-09-929-818-99	Sequence 99, Appl
449	3	8.8	28	9	US-09-929-818-100	Sequence 100, App
450	3	8.8	28	9	US-09-929-818-101	Sequence 101, App
451	3	8.8	28	9	US-09-929-818-102	Sequence 102, App
452	3	8.8	28	9	US-09-929-818-103	Sequence 103, App
453	3	8.8	28	9	US-09-929-818-104	Sequence 104, App
454	3	8.8	28	9	US-09-929-818-105	Sequence 105, App
455	3	8.8	28	9	US-09-929-818-106	Sequence 106, App

456	3	8.8	28	9	US-09-929-818-107	Sequence 107, App
457	3	8.8	28	9	US-09-929-818-108	Sequence 108, App
458	3	8.8	28	9	US-09-929-818-109	Sequence 109, App
459	3	8.8	28	9	US-09-929-818-110	Sequence 110, App
460	3	8.8	28	9	US-09-929-818-111	Sequence 111, App
461	3	8.8	28	9	US-09-929-818-112	Sequence 112, App
462	3	8.8	28	9	US-09-929-818-113	Sequence 113, App
463	3	8.8	28	9	US-09-929-818-114	Sequence 114, App
464	3	8.8	28	9	US-09-929-818-115	Sequence 115, App
465	3	8.8	28	9	US-09-929-818-116	Sequence 116, App
466	3	8.8	28	9	US-09-929-818-117	Sequence 117, App
467	3	8.8	28	9	US-09-929-818-118	Sequence 118, App
468	3	8.8	28	9	US-09-929-818-119	Sequence 119, App
469	3	8.8	28	9	US-09-929-818-120	Sequence 120, App
470	3	8.8	28	9	US-09-929-818-121	Sequence 121, App
471	3	8.8	28	9	US-09-929-818-123	Sequence 123, App
472	3	8.8	28	9	US-09-929-818-124	Sequence 124, App
473	3	8.8	28	9	US-09-929-818-125	Sequence 125, App
474	3	8.8	28	9	US-09-929-818-126	Sequence 126, App
475	3	8.8	28	9	US-09-929-818-127	Sequence 127, App
476	3	8.8	28	9	US-09-929-818-128	Sequence 128, App
477	3	8.8	28	9	US-09-929-818-129	Sequence 129, App
478	3	8.8	28	9	US-09-929-818-130	Sequence 130, App
479	3	8.8	28	9	US-09-929-818-131	Sequence 131, App
480	3	8.8	28	9	US-09-929-818-132	Sequence 132, App
481	3	8.8	28	9	US-09-929-818-133	Sequence 133, App
482	3	8.8	28	9	US-09-929-818-134	Sequence 134, App
483	3	8.8	28	9	US-09-929-818-135	Sequence 135, App
484	3	8.8	28	9	US-09-929-818-136	Sequence 136, App
485	3	8.8	28	9	US-09-929-818-137	Sequence 137, App
486	3	8.8	28	9	US-09-929-818-138	Sequence 138, App
487	3	8.8	28	9	US-09-929-818-139	Sequence 139, App
488	3	8.8	28	9	US-09-929-818-140	Sequence 140, App
489	3	8.8	28	9	US-09-929-818-141	Sequence 141, App
490	3	8.8	28	9	US-09-929-818-142	Sequence 142, App
491	3	8.8	28	9	US-09-929-818-143	Sequence 143, App
492	3	8.8	28	9	US-09-929-818-144	Sequence 144, App
493	3	8.8	28	9	US-09-929-818-145	Sequence 145, App
494	3	8.8	28	9	US-09-929-818-146	Sequence 146, App
495	3	8.8	28	9	US-09-929-818-147	Sequence 147, App
496	3	8.8	28	9	US-09-929-818-148	Sequence 148, App
497	3	8.8	28	9	US-09-929-818-149	Sequence 149, App
498	3	8.8	28	9	US-09-929-818-150	Sequence 150, App
499	3	8.8	28	9	US-09-929-818-151	Sequence 151, App
500	3	8.8	28	9	US-09-929-818-152	Sequence 152, App
501	3	8.8	28	9	US-09-929-818-153	Sequence 153, App
502	3	8.8	28	9	US-09-929-818-154	Sequence 154, App
503	3	8.8	28	9	US-09-929-818-155	Sequence 155, App
504	3	8.8	28	9	US-09-929-818-156	Sequence 156, App
505	3	8.8	28	9	US-09-929-818-157	Sequence 157, App
506	3	8.8	28	9	US-09-929-818-158	Sequence 158, App
507	3	8.8	28	9	US-09-929-818-159	Sequence 159, App
508	3	8.8	28	9	US-09-929-818-160	Sequence 160, App
509	3	8.8	28	9	US-09-929-818-161	Sequence 161, App
510	3	8.8	28	9	US-09-929-818-162	Sequence 162, App
511	3	8.8	28	9	US-09-929-818-163	Sequence 163, App
512	3	8.8	28	9	US-09-929-818-164	Sequence 164, App

513	3	8.8	28	9	US-09-929-818-165	Sequence 165, App
514	3	8.8	28	9	US-09-929-818-166	Sequence 166, App
515	3	8.8	28	9	US-09-929-818-167	Sequence 167, App
516	3	8.8	28	9	US-09-929-818-168	Sequence 168, App
517	3	8.8	28	9	US-09-929-818-169	Sequence 169, App
518	3	8.8	28	9	US-09-929-818-170	Sequence 170, App
519	3	8.8	28	9	US-09-929-818-171	Sequence 171, App
520	3	8.8	28	9	US-09-929-818-172	Sequence 172, App
521	3	8.8	28	9	US-09-929-818-173	Sequence 173, App
522	3	8.8	28	9	US-09-929-818-174	Sequence 174, App
523	3	8.8	28	9	US-09-929-818-175	Sequence 175, App
524	3	8.8	28	9	US-09-929-818-176	Sequence 176, App
525	3	8.8	28	9	US-09-929-818-177	Sequence 177, App
526	3	8.8	28	9	US-09-929-818-178	Sequence 178, App
527	3	8.8	28	9	US-09-929-818-179	Sequence 179, App
528	3	8.8	28	9	US-09-929-818-180	Sequence 180, App
529	3	8.8	28	9	US-09-929-818-181	Sequence 181, App
530	3	8.8	28	9	US-09-929-818-182	Sequence 182, App
531	3	8.8	28	9	US-09-929-818-183	Sequence 183, App
532	3	8.8	28	9	US-09-929-818-184	Sequence 184, App
533	3	8.8	28	9	US-09-929-818-185	Sequence 185, App
534	3	8.8	28	9	US-09-929-818-186	Sequence 186, App
535	3	8.8	28	9	US-09-929-818-187	Sequence 187, App
536	3	8.8	28	9	US-09-929-818-188	Sequence 188, App
537	3	8.8	28	9	US-09-929-818-189	Sequence 189, App
538	3	8.8	28	9	US-09-929-818-190	Sequence 190, App
539	3	8.8	28	9	US-09-929-818-191	Sequence 191, App
540	3	8.8	28	9	US-09-929-818-192	Sequence 192, App
541	3	8.8	28	9	US-09-929-818-193	Sequence 193, App
542	3	8.8	28	9	US-09-929-818-194	Sequence 194, App
543	3	8.8	28	9	US-09-929-818-195	Sequence 195, App
544	3	8.8	28	9	US-09-929-818-196	Sequence 196, App
545	3	8.8	28	9	US-09-929-818-197	Sequence 197, App
546	3	8.8	28	9	US-09-929-818-198	Sequence 198, App
547	3	8.8	28	9	US-09-929-818-199	Sequence 199, App
548	3	8.8	28	9	US-09-929-818-201	Sequence 201, App
549	3	8.8	28	9	US-09-929-818-202	Sequence 202, App
550	3	8.8	28	9	US-09-929-818-207	Sequence 207, App
551	3	8.8	28	10	US-09-117-380B-4	Sequence 4, Appli
552	3	8.8	28	10	US-09-003-869-40	Sequence 40, Appl
553	3	8.8	28	10	US-09-003-869-90	Sequence 90, Appl
554	3	8.8	28	10	US-09-003-869-91	Sequence 91, Appl
555	3	8.8	28	10	US-09-003-869-92	Sequence 92, Appl
556	3	8.8	28	10	US-09-003-869-95	Sequence 95, Appl
557	3	8.8	28	10	US-09-003-869-104	Sequence 104, App
558	3	8.8	28	10	US-09-003-869-105	Sequence 105, App
559	3	8.8	28	10	US-09-003-869-106	Sequence 106, App
560	3	8.8	28	10	US-09-003-869-107	Sequence 107, App
561	3	8.8	28	10	US-09-003-869-108	Sequence 108, App
562	3	8.8	28	10	US-09-003-869-109	Sequence 109, App
563	3	8.8	28	10	US-09-003-869-111	Sequence 111, App
564	3	8.8	28	10	US-09-003-869-113	Sequence 113, App
565	3	8.8	28	10	US-09-003-869-115	Sequence 115, App
566	3	8.8	28	10	US-09-003-869-117	Sequence 117, App
567	3	8.8	28	10	US-09-003-869-119	Sequence 119, App
568	3	8.8	28	10	US-09-003-869-121	Sequence 121, App
569	3	8.8	28	10	US-09-003-869-123	Sequence 123, App

570	3	8.8	28	10	US-09-003-869-125	Sequence 125, App
571	3	8.8	28	10	US-09-003-869-127	Sequence 127, App
572	3	8.8	28	10	US-09-003-869-129	Sequence 129, App
573	3	8.8	28	10	US-09-003-869-131	Sequence 131, App
574	3	8.8	28	10	US-09-003-869-133	Sequence 133, App
575	3	8.8	28	10	US-09-003-869-135	Sequence 135, App
576	3	8.8	28	10	US-09-003-869-137	Sequence 137, App
577	3	8.8	28	10	US-09-003-869-139	Sequence 139, App
578	3	8.8	28	10	US-09-003-869-141	Sequence 141, App
579	3	8.8	28	10	US-09-003-869-143	Sequence 143, App
580	3	8.8	28	10	US-09-003-869-145	Sequence 145, App
581	3	8.8	28	10	US-09-003-869-147	Sequence 147, App
582	3	8.8	28	10	US-09-003-869-149	Sequence 149, App
583	3	8.8	28	10	US-09-003-869-151	Sequence 151, App
584	3	8.8	28	10	US-09-003-869-155	Sequence 155, App
585	3	8.8	28	10	US-09-003-869-163	Sequence 163, App
586	3	8.8	28	10	US-09-003-869-165	Sequence 165, App
587	3	8.8	28	10	US-09-903-456-116	Sequence 116, App
588	3	8.8	28	10	US-09-989-903-23	Sequence 23, Appl
589	3	8.8	28	10	US-09-880-149-10	Sequence 10, Appl
590	3	8.8	28	10	US-09-880-149-11	Sequence 11, Appl
591	3	8.8	28	10	US-09-986-552-27	Sequence 27, Appl
592	3	8.8	28	10	US-09-934-060A-20	Sequence 20, Appl
593	3	8.8	28	10	US-09-999-745-53	Sequence 53, Appl
594	3	8.8	28	10	US-09-981-876-241	Sequence 241, App
595	3	8.8	28	10	US-09-880-498-1	Sequence 1, Appli
596	3	8.8	28	10	US-09-554-000-37	Sequence 37, Appl
597	3	8.8	28	10	US-09-880-132-10	Sequence 10, Appl
598	3	8.8	28	10	US-09-880-132-11	Sequence 11, Appl
599	3	8.8	28	10	US-09-848-967-3	Sequence 3, Appli
600	3	8.8	28	10	US-09-848-967-4	Sequence 4, Appli
601	3	8.8	28	10	US-09-976-740-26	Sequence 26, Appl
602	3	8.8	28	11	US-09-983-802-481	Sequence 481, App
603	3	8.8	28	11	US-09-983-802-531	Sequence 531, App
604	3	8.8	28	11	US-09-999-724-28	Sequence 28, Appl
605	3	8.8	28	11	US-09-148-545-241	Sequence 241, App
606	3	8.8	28	11	US-09-974-879-269	Sequence 269, App
607	3	8.8	28	11	US-09-974-879-520	Sequence 520, App
608	3	8.8	28	11	US-09-974-879-543	Sequence 543, App
609	3	8.8	28	11	US-09-974-879-579	Sequence 579, App
610	3	8.8	28	11	US-09-756-690A-40	Sequence 40, Appl
611	3	8.8	28	11	US-09-756-690A-90	Sequence 90, Appl
612	3	8.8	28	11	US-09-756-690A-91	Sequence 91, Appl
613	3	8.8	28	11	US-09-756-690A-92	Sequence 92, Appl
614	3	8.8	28	11	US-09-756-690A-95	Sequence 95, Appl
615	3	8.8	28	11	US-09-756-690A-104	Sequence 104, App
616	3	8.8	28	11	US-09-756-690A-105	Sequence 105, App
617	3	8.8	28	11	US-09-756-690A-106	Sequence 106, App
618	3	8.8	28	11	US-09-756-690A-107	Sequence 107, App
619	3	8.8	28	11	US-09-756-690A-108	Sequence 108, App
620	3	8.8	28	11	US-09-756-690A-109	Sequence 109, App
621	3	8.8	28	11	US-09-756-690A-111	Sequence 111, App
622	3	8.8	28	11	US-09-756-690A-113	Sequence 113, App
623	3	8.8	28	11	US-09-756-690A-115	Sequence 115, App
624	3	8.8	28	11	US-09-756-690A-117	Sequence 117, App
625	3	8.8	28	11	US-09-756-690A-119	Sequence 119, App
626	3	8.8	28	11	US-09-756-690A-121	Sequence 121, App

627	3	8.8	28	11	US-09-756-690A-123	Sequence 123, App
628	3	8.8	28	11	US-09-756-690A-125	Sequence 125, App
629	3	8.8	28	11	US-09-756-690A-127	Sequence 127, App
630	3	8.8	28	11	US-09-756-690A-129	Sequence 129, App
631	3	8.8	28	11	US-09-756-690A-131	Sequence 131, App
632	3	8.8	28	11	US-09-756-690A-133	Sequence 133, App
633	3	8.8	28	11	US-09-756-690A-135	Sequence 135, App
634	3	8.8	28	11	US-09-756-690A-137	Sequence 137, App
635	3	8.8	28	11	US-09-756-690A-139	Sequence 139, App
636	3	8.8	28	11	US-09-756-690A-141	Sequence 141, App
637	3	8.8	28	11	US-09-756-690A-143	Sequence 143, App
638	3	8.8	28	11	US-09-756-690A-145	Sequence 145, App
639	3	8.8	28	11	US-09-756-690A-147	Sequence 147, App
640	3	8.8	28	11	US-09-756-690A-149	Sequence 149, App
641	3	8.8	28	11	US-09-756-690A-151	Sequence 151, App
642	3	8.8	28	11	US-09-756-690A-155	Sequence 155, App
643	3	8.8	28	11	US-09-756-690A-163	Sequence 163, App
644	3	8.8	28	11	US-09-756-690A-165	Sequence 165, App
645	3	8.8	28	11	US-09-843-221A-72	Sequence 72, Appl
646	3	8.8	28	11	US-09-843-221A-75	Sequence 75, Appl
647	3	8.8	28	11	US-09-843-221A-104	Sequence 104, App
648	3	8.8	28	11	US-09-925-299-1173	Sequence 1173, Ap
649	3	8.8	28	11	US-09-945-917-23	Sequence 23, Appl
650	3	8.8	28	11	US-09-813-153-220	Sequence 220, App
651	3	8.8	28	11	US-09-876-904A-230	Sequence 230, App
652	3	8.8	28	11	US-09-892-877-335	Sequence 335, App
653	3	8.8	28	11	US-09-910-180-19	Sequence 19, Appl
654	3	8.8	28	11	US-09-899-495-104	Sequence 104, App
655	3	8.8	28	11	US-09-305-736-285	Sequence 285, App
656	3	8.8	28	11	US-09-305-736-522	Sequence 522, App
657	3	8.8	28	11	US-09-305-736-545	Sequence 545, App
658	3	8.8	28	11	US-09-305-736-580	Sequence 580, App
659	3	8.8	28	11	US-09-948-783-348	Sequence 348, App
660	3	8.8	28	11	US-09-866-066-31	Sequence 31, Appl
661	3	8.8	28	12	US-10-195-730-307	Sequence 307, App
662	3	8.8	28	12	US-10-195-730-354	Sequence 354, App
663	3	8.8	28	12	US-10-309-422-4	Sequence 4, Appli
664	3	8.8	28	12	US-10-334-405-4	Sequence 4, Appli
665	3	8.8	28	12	US-10-251-703-21	Sequence 21, Appl
666	3	8.8	28	12	US-10-306-686-27	Sequence 27, Appl
667	3	8.8	28	12	US-09-991-225-35	Sequence 35, Appl
668	3	8.8	28	12	US-10-100-256B-1	Sequence 1, Appli
669	3	8.8	28	12	US-10-345-281-10	Sequence 10, Appl
670	3	8.8	28	12	US-10-345-281-11	Sequence 11, Appl
671	3	8.8	28	12	US-10-254-569A-1	Sequence 1, Appli
672	3	8.8	28	12	US-10-254-569A-2	Sequence 2, Appli
673	3	8.8	28	12	US-10-254-569A-3	Sequence 3, Appli
674	3	8.8	28	12	US-10-254-569A-4	Sequence 4, Appli
675	3	8.8	28	12	US-10-254-569A-5	Sequence 5, Appli
676	3	8.8	28	12	US-10-254-569A-6	Sequence 6, Appli
677	3	8.8	28	12	US-10-254-569A-7	Sequence 7, Appli
678	3	8.8	28	12	US-10-254-569A-8	Sequence 8, Appli
679	3	8.8	28	12	US-10-254-569A-9	Sequence 9, Appli
680	3	8.8	28	12	US-10-254-569A-10	Sequence 10, Appl
681	3	8.8	28	12	US-10-254-569A-11	Sequence 11, Appl
682	3	8.8	28	12	US-10-254-569A-12	Sequence 12, Appl
683	3	8.8	28	12	US-10-156-911-116	Sequence 116, App

684	3	8.8	28	12	US-09-845-917A-23	Sequence 23, Appl
685	3	8.8	28	12	US-10-322-746-7	Sequence 7, Appli
686	3	8.8	28	12	US-10-411-224-108	Sequence 108, App
687	3	8.8	28	12	US-09-829-922-22	Sequence 22, Appl
688	3	8.8	28	12	US-10-231-417-466	Sequence 466, App
689	3	8.8	28	12	US-10-231-417-591	Sequence 591, App
690	3	8.8	28	12	US-10-312-691-2	Sequence 2, Appli
691	3	8.8	28	12	US-10-314-506-16	Sequence 16, Appl
692	3	8.8	28	12	US-10-314-506-17	Sequence 17, Appl
693	3	8.8	28	12	US-10-408-736-81	Sequence 81, Appl
694	3	8.8	28	12	US-09-933-767-626	Sequence 626, App
695	3	8.8	28	12	US-09-933-767-1089	Sequence 1089, Ap
696	3	8.8	28	12	US-10-105-232-329	Sequence 329, App
697	3	8.8	28	12	US-10-131-686A-19	Sequence 19, Appl
698	3	8.8	28	12	US-10-289-135A-36	Sequence 36, Appl
699	3	8.8	28	12	US-10-276-392-1	Sequence 1, Appli
700	3	8.8	28	12	US-10-276-392-7	Sequence 7, Appli
701	3	8.8	28	12	US-10-276-392-8	Sequence 8, Appli
702	3	8.8	28	12	US-10-276-392-9	Sequence 9, Appli
703	3	8.8	28	12	US-10-276-392-10	Sequence 10, Appl
704	3	8.8	28	12	US-10-276-392-11	Sequence 11, Appl
705	3	8.8	28	12	US-10-276-392-12	Sequence 12, Appl
706	3	8.8	28	12	US-10-276-392-13	Sequence 13, Appl
707	3	8.8	28	12	US-10-276-392-14	Sequence 14, Appl
708	3	8.8	28	12	US-10-276-392-15	Sequence 15, Appl
709	3	8.8	28	12	US-10-276-392-16	Sequence 16, Appl
710	3	8.8	28	12	US-10-276-392-17	Sequence 17, Appl
711	3	8.8	28	12	US-10-276-392-18	Sequence 18, Appl
712	3	8.8	28	12	US-10-276-392-19	Sequence 19, Appl
713	3	8.8	28	12	US-10-276-392-20	Sequence 20, Appl
714	3	8.8	28	12	US-10-276-392-21	Sequence 21, Appl
715	3	8.8	28	12	US-10-330-872-9	Sequence 9, Appli
716	3	8.8	28	12	US-10-351-641-54	Sequence 54, Appl
717	3	8.8	28	12	US-10-351-641-62	Sequence 62, Appl
718	3	8.8	28	12	US-10-351-641-982	Sequence 982, App
719	3	8.8	28	12	US-10-351-641-1279	Sequence 1279, Ap
720	3	8.8	28	12	US-10-351-641-1280	Sequence 1280, Ap
721	3	8.8	28	12	US-10-351-641-1314	Sequence 1314, Ap
722	3	8.8	28	12	US-10-351-641-1315	Sequence 1315, Ap
723	3	8.8	28	12	US-10-351-641-1689	Sequence 1689, Ap
724	3	8.8	28	12	US-10-029-386-28154	Sequence 28154, A
725	3	8.8	28	12	US-10-029-386-28548	Sequence 28548, A
726	3	8.8	28	12	US-10-029-386-29937	Sequence 29937, A
727	3	8.8	28	12	US-10-029-386-31090	Sequence 31090, A
728	3	8.8	28	12	US-10-029-386-31138	Sequence 31138, A
729	3	8.8	28	12	US-10-029-386-31267	Sequence 31267, A
730	3	8.8	28	12	US-10-029-386-31429	Sequence 31429, A
731	3	8.8	28	12	US-10-029-386-33289	Sequence 33289, A
732	3	8.8	28	12	US-10-029-386-33582	Sequence 33582, A
733	3	8.8	28	12	US-10-189-437-316	Sequence 316, App
734	3	8.8	28	12	US-10-189-437-669	Sequence 669, App
735	3	8.8	28	12	US-10-080-254-100	Sequence 100, App
736	3	8.8	28	12	US-10-080-608A-1	Sequence 1, Appli
737	3	8.8	28	12	US-09-818-683-285	Sequence 285, App
738	3	8.8	28	12	US-09-818-683-522	Sequence 522, App
739	3	8.8	28	12	US-09-818-683-545	Sequence 545, App
740	3	8.8	28	12	US-09-818-683-580	Sequence 580, App

741	3	8.8	28	12	US-10-370-685-90	Sequence 90, Appl
742	3	8.8	28	12	US-09-873-155-43	Sequence 43, Appl
743	3	8.8	28	12	US-10-366-493-24	Sequence 24, Appl
744	3	8.8	28	12	US-10-391-399-86	Sequence 86, Appl
745	3	8.8	28	12	US-10-211-689-8	Sequence 8, Appli
746	3	8.8	28	12	US-10-324-143-148	Sequence 148, App
747	3	8.8	28	12	US-10-242-355-646	Sequence 646, App
748	3	8.8	28	12	US-10-245-871-32	Sequence 32, Appl
749	3	8.8	28	12	US-10-154-884B-11082	Sequence 11082, A
750	3	8.8	28	12	US-10-264-049-2573	Sequence 2573, Ap
751	3	8.8	28	12	US-10-264-049-3158	Sequence 3158, Ap
752	3	8.8	28	14	US-10-014-269-16	Sequence 16, Appl
753	3	8.8	28	14	US-10-014-269-17	Sequence 17, Appl
754	3	8.8	28	14	US-10-023-529-26	Sequence 26, Appl
755	3	8.8	28	14	US-10-105-931-19	Sequence 19, Appl
756	3	8.8	28	14	US-10-105-931-23	Sequence 23, Appl
757	3	8.8	28	14	US-10-090-109A-1	Sequence 1, Appli
758	3	8.8	28	14	US-10-023-523-26	Sequence 26, Appl
759	3	8.8	28	14	US-10-044-722-8	Sequence 8, Appli
760	3	8.8	28	14	US-10-002-974-16	Sequence 16, Appl
761	3	8.8	28	14	US-10-002-974-17	Sequence 17, Appl
762	3	8.8	28	14	US-10-118-984-19	Sequence 19, Appl
763	3	8.8	28	14	US-10-118-984-23	Sequence 23, Appl
764	3	8.8	28	15	US-10-014-162-48	Sequence 48, Appl
765	3	8.8	28	15	US-10-210-895-9	Sequence 9, Appli
766	3	8.8	28	15	US-10-000-256A-219	Sequence 219, App
767	3	8.8	28	15	US-10-068-564-23	Sequence 23, Appl
768	3	8.8	28	15	US-10-078-090-126	Sequence 126, App
769	3	8.8	28	15	US-10-004-530A-17	Sequence 17, Appl
770	3	8.8	28	15	US-10-131-433-6	Sequence 6, Appli
771	3	8.8	28	15	US-10-097-065-486	Sequence 486, App
772	3	8.8	28	15	US-10-097-065-598	Sequence 598, App
773	3	8.8	28	15	US-10-216-556-14	Sequence 14, Appl
774	3	8.8	28	15	US-10-059-261-324	Sequence 324, App
775	3	8.8	28	15	US-10-150-111-131	Sequence 131, App
776	3	8.8	28	15	US-10-211-994-1	Sequence 1, Appli
777	3	8.8	28	15	US-10-157-224A-40	Sequence 40, Appl
778	3	8.8	28	15	US-10-157-224A-90	Sequence 90, Appl
779	3	8.8	28	15	US-10-157-224A-91	Sequence 91, Appl
780	3	8.8	28	15	US-10-157-224A-92	Sequence 92, Appl
781	3	8.8	28	15	US-10-157-224A-95	Sequence 95, Appl
782	3	8.8	28	15	US-10-157-224A-104	Sequence 104, App
783	3	8.8	28	15	US-10-157-224A-105	Sequence 105, App
784	3	8.8	28	15	US-10-157-224A-106	Sequence 106, App
785	3	8.8	28	15	US-10-157-224A-107	Sequence 107, App
786	3	8.8	28	15	US-10-157-224A-108	Sequence 108, App
787	3	8.8	28	15	US-10-157-224A-109	Sequence 109, App
788	3	8.8	28	15	US-10-157-224A-111	Sequence 111, App
789	3	8.8	28	15	US-10-157-224A-113	Sequence 113, App
790	3	8.8	28	15	US-10-157-224A-115	Sequence 115, App
791	3	8.8	28	15	US-10-157-224A-117	Sequence 117, App
792	3	8.8	28	15	US-10-157-224A-119	Sequence 119, App
793	3	8.8	28	15	US-10-157-224A-121	Sequence 121, App
794	3	8.8	28	15	US-10-157-224A-123	Sequence 123, App
795	3	8.8	28	15	US-10-157-224A-125	Sequence 125, App
796	3	8.8	28	15	US-10-157-224A-127	Sequence 127, App
797	3	8.8	28	15	US-10-157-224A-129	Sequence 129, App

798	3	8.8	28	15	US-10-157-224A-131	Sequence 131, App
799	3	8.8	28	15	US-10-157-224A-133	Sequence 133, App
800	3	8.8	28	15	US-10-157-224A-135	Sequence 135, App
801	3	8.8	28	15	US-10-157-224A-137	Sequence 137, App
802	3	8.8	28	15	US-10-157-224A-139	Sequence 139, App
803	3	8.8	28	15	US-10-157-224A-141	Sequence 141, App
804	3	8.8	28	15	US-10-157-224A-143	Sequence 143, App
805	3	8.8	28	15	US-10-157-224A-145	Sequence 145, App
806	3	8.8	28	15	US-10-157-224A-147	Sequence 147, App
807	3	8.8	28	15	US-10-157-224A-149	Sequence 149, App
808	3	8.8	28	15	US-10-157-224A-151	Sequence 151, App
809	3	8.8	28	15	US-10-157-224A-155	Sequence 155, App
810	3	8.8	28	15	US-10-157-224A-163	Sequence 163, App
811	3	8.8	28	15	US-10-157-224A-165	Sequence 165, App
812	3	8.8	28	15	US-10-187-051-40	Sequence 40, Appl
813	3	8.8	28	15	US-10-187-051-90	Sequence 90, Appl
814	3	8.8	28	15	US-10-187-051-91	Sequence 91, Appl
815	3	8.8	28	15	US-10-187-051-92	Sequence 92, Appl
816	3	8.8	28	15	US-10-187-051-95	Sequence 95, Appl
817	3	8.8	28	15	US-10-187-051-104	Sequence 104, App
818	3	8.8	28	15	US-10-187-051-105	Sequence 105, App
819	3	8.8	28	15	US-10-187-051-106	Sequence 106, App
820	3	8.8	28	15	US-10-187-051-107	Sequence 107, App
821	3	8.8	28	15	US-10-187-051-108	Sequence 108, App
822	3	8.8	28	15	US-10-187-051-109	Sequence 109, App
823	3	8.8	28	15	US-10-187-051-111	Sequence 111, App
824	3	8.8	28	15	US-10-187-051-113	Sequence 113, App
825	3	8.8	28	15	US-10-187-051-115	Sequence 115, App
826	3	8.8	28	15	US-10-187-051-117	Sequence 117, App
827	3	8.8	28	15	US-10-187-051-119	Sequence 119, App
828	3	8.8	28	15	US-10-187-051-121	Sequence 121, App
829	3	8.8	28	15	US-10-187-051-123	Sequence 123, App
830	3	8.8	28	15	US-10-187-051-125	Sequence 125, App
831	3	8.8	28	15	US-10-187-051-127	Sequence 127, App
832	3	8.8	28	15	US-10-187-051-129	Sequence 129, App
833	3	8.8	28	15	US-10-187-051-131	Sequence 131, App
834	3	8.8	28	15	US-10-187-051-133	Sequence 133, App
835	3	8.8	28	15	US-10-187-051-135	Sequence 135, App
836	3	8.8	28	15	US-10-187-051-137	Sequence 137, App
837	3	8.8	28	15	US-10-187-051-139	Sequence 139, App
838	3	8.8	28	15	US-10-187-051-141	Sequence 141, App
839	3	8.8	28	15	US-10-187-051-143	Sequence 143, App
840	3	8.8	28	15	US-10-187-051-145	Sequence 145, App
841	3	8.8	28	15	US-10-187-051-147	Sequence 147, App
842	3	8.8	28	15	US-10-187-051-149	Sequence 149, App
843	3	8.8	28	15	US-10-187-051-151	Sequence 151, App
844	3	8.8	28	15	US-10-187-051-155	Sequence 155, App
845	3	8.8	28	15	US-10-187-051-163	Sequence 163, App
846	3	8.8	28	15	US-10-187-051-165	Sequence 165, App
847	3	8.8	28	15	US-10-023-282-626	Sequence 626, App
848	3	8.8	28	15	US-10-023-282-1089	Sequence 1089, Ap
849	3	8.8	28	15	US-10-255-532-6	Sequence 6, Appli
850	3	8.8	28	15	US-10-075-869-24	Sequence 24, Appl
851	3	8.8	28	15	US-10-202-724-3	Sequence 3, Appli
852	3	8.8	28	15	US-10-262-017-3	Sequence 3, Appli
853	3	8.8	28	15	US-10-106-698-5608	Sequence 5608, Ap
854	3	8.8	28	15	US-10-106-698-6764	Sequence 6764, Ap

855	3	8.8	28	15	US-10-106-698-7736	Sequence 7736, Ap
856	3	8.8	28	15	US-10-106-698-7875	Sequence 7875, Ap
857	3	8.8	28	15	US-10-106-698-8447	Sequence 8447, Ap
858	3	8.8	28	15	US-10-192-283A-12	Sequence 12, Appl
859	3	8.8	28	15	US-10-197-954-62	Sequence 62, Appl
860	3	8.8	28	15	US-10-197-954-145	Sequence 145, App
861	3	8.8	28	15	US-10-283-500-19	Sequence 19, Appl
862	3	8.8	28	15	US-10-295-981-19	Sequence 19, Appl
863	3	8.8	28	15	US-10-295-981-23	Sequence 23, Appl
864	3	8.8	28	15	US-10-198-053-598	Sequence 598, App
865	3	8.8	28	15	US-10-160-290-22	Sequence 22, Appl
866	3	8.8	29	8	US-08-913-430-4	Sequence 4, Appli
867	3	8.8	29	9	US-09-205-658-71	Sequence 71, Appl
868	3	8.8	29	9	US-09-730-379B-4	Sequence 4, Appli
869	3	8.8	29	9	US-09-765-527-13	Sequence 13, Appl
870	3	8.8	29	9	US-09-765-527-64	Sequence 64, Appl
871	3	8.8	29	9	US-09-005-243-73	Sequence 73, Appl
872	3	8.8	29	9	US-09-224-683-73	Sequence 73, Appl
873	3	8.8	29	9	US-09-932-161-1	Sequence 1, Appli
874	3	8.8	29	9	US-09-844-353A-71	Sequence 71, Appl
875	3	8.8	29	9	US-09-864-761-33834	Sequence 33834, A
876	3	8.8	29	9	US-09-864-761-34011	Sequence 34011, A
877	3	8.8	29	9	US-09-864-761-34337	Sequence 34337, A
878	3	8.8	29	9	US-09-864-761-36235	Sequence 36235, A
879	3	8.8	29	9	US-09-864-761-37068	Sequence 37068, A
880	3	8.8	29	9	US-09-864-761-37355	Sequence 37355, A
881	3	8.8	29	9	US-09-864-761-37579	Sequence 37579, A
882	3	8.8	29	9	US-09-864-761-37814	Sequence 37814, A
883	3	8.8	29	9	US-09-864-761-37955	Sequence 37955, A
884	3	8.8	29	9	US-09-864-761-38222	Sequence 38222, A
885	3	8.8	29	9	US-09-864-761-38638	Sequence 38638, A
886	3	8.8	29	9	US-09-864-761-38968	Sequence 38968, A
887	3	8.8	29	9	US-09-864-761-39320	Sequence 39320, A
888	3	8.8	29	9	US-09-864-761-40067	Sequence 40067, A
889	3	8.8	29	9	US-09-864-761-40393	Sequence 40393, A
890	3	8.8	29	9	US-09-864-761-40727	Sequence 40727, A
891	3	8.8	29	9	US-09-864-761-40944	Sequence 40944, A
892	3	8.8	29	9	US-09-864-761-41199	Sequence 41199, A
893	3	8.8	29	9	US-09-864-761-41596	Sequence 41596, A
894	3	8.8	29	9	US-09-864-761-42035	Sequence 42035, A
895	3	8.8	29	9	US-09-864-761-42321	Sequence 42321, A
896	3	8.8	29	9	US-09-864-761-42342	Sequence 42342, A
897	3	8.8	29	9	US-09-864-761-42467	Sequence 42467, A
898	3	8.8	29	9	US-09-864-761-42588	Sequence 42588, A
899	3	8.8	29	9	US-09-864-761-42832	Sequence 42832, A
900	3	8.8	29	9	US-09-864-761-42924	Sequence 42924, A
901	3	8.8	29	9	US-09-864-761-43064	Sequence 43064, A
902	3	8.8	29	9	US-09-864-761-43635	Sequence 43635, A
903	3	8.8	29	9	US-09-864-761-44480	Sequence 44480, A
904	3	8.8	29	9	US-09-864-761-44716	Sequence 44716, A
905	3	8.8	29	9	US-09-864-761-44947	Sequence 44947, A
906	3	8.8	29	9	US-09-864-761-45036	Sequence 45036, A
907	3	8.8	29	9	US-09-864-761-45581	Sequence 45581, A
908	3	8.8	29	9	US-09-864-761-45777	Sequence 45777, A
909	3	8.8	29	9	US-09-864-761-45815	Sequence 45815, A
910	3	8.8	29	9	US-09-864-761-45948	Sequence 45948, A
911	3	8.8	29	9	US-09-864-761-46618	Sequence 46618, A

912	3	8.8	29	9	US-09-864-761-47028	Sequence 47028, A
913	3	8.8	29	9	US-09-864-761-47383	Sequence 47383, A
914	3	8.8	29	9	US-09-864-761-47524	Sequence 47524, A
915	3	8.8	29	9	US-09-864-761-48176	Sequence 48176, A
916	3	8.8	29	9	US-09-864-761-48505	Sequence 48505, A
917	3	8.8	29	9	US-09-864-761-48518	Sequence 48518, A
918	3	8.8	29	9	US-09-864-761-48746	Sequence 48746, A
919	3	8.8	29	9	US-09-876-388-22	Sequence 22, Appl
920	3	8.8	29	9	US-09-925-299-1270	Sequence 1270, Ap
921	3	8.8	29	9	US-09-764-869-638	Sequence 638, App
922	3	8.8	29	9	US-09-764-869-674	Sequence 674, App
923	3	8.8	29	9	US-09-881-490-3	Sequence 3, Appli
924	3	8.8	29	9	US-09-789-836-13	Sequence 13, Appl
925	3	8.8	29	10	US-09-927-112-5	Sequence 5, Appli
926	3	8.8	29	10	US-09-927-112-6	Sequence 6, Appli
927	3	8.8	29	10	US-09-872-864-17	Sequence 17, Appl
928	3	8.8	29	10	US-09-872-864-18	Sequence 18, Appl
929	3	8.8	29	10	US-09-872-864-19	Sequence 19, Appl
930	3	8.8	29	10	US-09-872-864-20	Sequence 20, Appl
931	3	8.8	29	10	US-09-922-261-258	Sequence 258, App
932	3	8.8	29	10	US-09-908-664-8	Sequence 8, Appli
933	3	8.8	29	10	US-09-908-664-9	Sequence 9, Appli
934	3	8.8	29	10	US-09-908-664-18	Sequence 18, Appl
935	3	8.8	29	10	US-09-905-831-12	Sequence 12, Appl
936	3	8.8	29	10	US-09-905-831-15	Sequence 15, Appl
937	3	8.8	29	10	US-09-003-869-79	Sequence 79, Appl
938	3	8.8	29	10	US-09-003-869-98	Sequence 98, Appl
939	3	8.8	29	10	US-09-885-441-12	Sequence 12, Appl
940	3	8.8	29	10	US-09-880-149-52	Sequence 52, Appl
941	3	8.8	29	10	US-09-880-149-55	Sequence 55, Appl
942	3	8.8	29	10	US-09-764-877-1395	Sequence 1395, Ap
943	3	8.8	29	10	US-09-867-852-152	Sequence 152, App
944	3	8.8	29	10	US-09-071-838-189	Sequence 189, App
945	3	8.8	29	10	US-09-071-838-242	Sequence 242, App
946	3	8.8	29	10	US-09-956-206A-1	Sequence 1, Appli
947	3	8.8	29	10	US-09-880-132-52	Sequence 52, Appl
948	3	8.8	29	10	US-09-880-132-55	Sequence 55, Appl
949	3	8.8	29	11	US-09-956-940-38	Sequence 38, Appl
950	3	8.8	29	11	US-09-974-879-406	Sequence 406, App
951	3	8.8	29	11	US-09-974-879-511	Sequence 511, App
952	3	8.8	29	11	US-09-974-879-527	Sequence 527, App
953	3	8.8	29	11	US-09-974-879-580	Sequence 580, App
954	3	8.8	29	11	US-09-259-658-15	Sequence 15, Appl
955	3	8.8	29	11	US-09-756-690A-79	Sequence 79, Appl
956	3	8.8	29	11	US-09-756-690A-98	Sequence 98, Appl
957	3	8.8	29	11	US-09-843-221A-152	Sequence 152, App
958	3	8.8	29	11	US-09-925-299-1270	Sequence 1270, Ap
959	3	8.8	29	11	US-09-813-153-218	Sequence 218, App
960	3	8.8	29	11	US-09-969-730-196	Sequence 196, App
961	3	8.8	29	11	US-09-876-904A-28	Sequence 28, Appl
962	3	8.8	29	11	US-09-764-891-4191	Sequence 4191, Ap
963	3	8.8	29	11	US-09-764-891-4851	Sequence 4851, Ap
964	3	8.8	29	11	US-09-847-208-125	Sequence 125, App
965	3	8.8	29	11	US-09-305-736-406	Sequence 406, App
966	3	8.8	29	11	US-09-305-736-512	Sequence 512, App
967	3	8.8	29	11	US-09-305-736-529	Sequence 529, App
968	3	8.8	29	11	US-09-305-736-581	Sequence 581, App

969	3	8.8	29	11	US-09-095-478-25	Sequence 25, Appl
970	3	8.8	29	11	US-09-908-139-19	Sequence 19, Appl
971	3	8.8	29	11	US-09-908-139-21	Sequence 21, Appl
972	3	8.8	29	11	US-09-491-614-14	Sequence 14, Appl
973	3	8.8	29	11	US-09-491-614-15	Sequence 15, Appl
974	3	8.8	29	11	US-09-910-082A-158	Sequence 158, App
975	3	8.8	29	11	US-09-910-082A-368	Sequence 368, App
976	3	8.8	29	12	US-10-153-604A-72	Sequence 72, Appl
977	3	8.8	29	12	US-10-199-869-87	Sequence 87, Appl
978	3	8.8	29	12	US-10-231-894-44	Sequence 44, Appl
979	3	8.8	29	12	US-10-345-281-52	Sequence 52, Appl
980	3	8.8	29	12	US-10-345-281-55	Sequence 55, Appl
981	3	8.8	29	12	US-10-234-816-95	Sequence 95, Appl
982	3	8.8	29	12	US-09-789-831-13	Sequence 13, Appl
983	3	8.8	29	12	US-09-935-384-757	Sequence 757, App
984	3	8.8	29	12	US-09-935-384-758	Sequence 758, App
985	3	8.8	29	12	US-10-131-909A-4	Sequence 4, Appli
986	3	8.8	29	12	US-10-131-909A-7	Sequence 7, Appli
987	3	8.8	29	12	US-10-096-777-1	Sequence 1, Appli
988	3	8.8	29	12	US-10-361-849-3	Sequence 3, Appli
989	3	8.8	29	12	US-10-008-524A-123	Sequence 123, App
990	3	8.8	29	12	US-10-340-458-4	Sequence 4, Appli
991	3	8.8	29	12	US-10-340-458-21	Sequence 21, Appl
992	3	8.8	29	12	US-09-933-767-1182	Sequence 1182, Ap
993	3	8.8	29	12	US-09-963-693-71	Sequence 71, Appl
994	3	8.8	29	12	US-10-105-232-319	Sequence 319, App
995	3	8.8	29	12	US-10-105-232-512	Sequence 512, App
996	3	8.8	29	12	US-10-280-066-334	Sequence 334, App
997	3	8.8	29	12	US-10-289-135A-25	Sequence 25, Appl
998	3	8.8	29	12	US-10-029-386-27545	Sequence 27545, A
999	3	8.8	29	12	US-10-029-386-27995	Sequence 27995, A
1000	3	8.8	29	12	US-10-029-386-29238	Sequence 29238, A

ALIGNMENTS

RESULT 1

US-09-843-221A-19

; Sequence 19, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

SVSEIOLMHNLGKHLNSMRBVEWLRKKLODVHNF 34

US-09-843-221A-42

Query Match 88.2%; Score 30; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.9e-24;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKLOD 30

US-09-843-221A-52

```

; Sequence 52, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;   APPLICANT: KOSTENUIK, PAUL
;   APPLICANT: LIU, CHUAN-FA
;   APPLICANT: LACEY, DAVID LEE
;   TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
;   TITLE OF INVENTION: RELATED PROTEIN
;   FILE REFERENCE: A-665B
;   CURRENT APPLICATION NUMBER: US/09/843,221A
;   CURRENT FILING DATE: 2001-04-26

```

; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-52

Query Match 52.9%; Score 18; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 5

US-09-843-221A-168

; Sequence 168, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain attached at the N-terminus through optional
linker
US-09-843-221A-168

Query Match 52.9%; Score 18; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e-12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 6

US-09-843-221A-51
; Sequence 51, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-51

Query Match 52.9%; Score 18; DB 11; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 7

US-09-843-221A-167
; Sequence 167, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN

```

; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain attached at the N-terminus through optional
linker
US-09-843-221A-167

```

```

Query Match          52.9%; Score 18; DB 11; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSM 18
        |||||
Db      1 SVSEIQLMHNLGKHLNSM 18

```

RESULT 8

```

US-09-843-221A-39
; Sequence 39, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: PRT

```


; ORGANISM: Homo sapiens
US-09-843-221A-39

Query Match 52.9%; Score 18; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 9

US-09-843-221A-50

; Sequence 50, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-50

Query Match 52.9%; Score 18; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 10

US-09-843-221A-124

; Sequence 124, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL

```

; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-124

```

```

Query Match          52.9%; Score 18; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSM 18
        |||||
Db      1 SVSEIQLMHNLGKHLNSM 18

```

RESULT 11

US-09-843-221A-125

```

; Sequence 125, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 30

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-125

Query Match 52.9%; Score 18; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
| | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 12

US-09-843-221A-126

; Sequence 126, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-126

Query Match 52.9%; Score 18; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
| | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 13

US-09-843-221A-127

; Sequence 127, Application US/09843221A

```

; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-127

```

```

Query Match          52.9%; Score 18; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSM 18
        |||||
Db      1 SVSEIQLMHNLGKHLNSM 18

```

RESULT 14

```

US-09-843-221A-166
; Sequence 166, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170

```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-166

Query Match 52.9%; Score 18; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 15

US-09-169-786-2
; Sequence 2, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-2

Query Match 52.9%; Score 18; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 16

US-09-843-221A-27
; Sequence 27, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA

```
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-27
```

```
Query Match          52.9%; Score 18; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SVSEIQLMHNLGKHLNSM 18
          |||||
Db       1 SVSEIQLMHNLGKHLNSM 18
```

RESULT 17

```
US-09-843-221A-28
; Sequence 28, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: modified human PTH
US-09-843-221A-28

Query Match 52.9%; Score 18; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 18

US-09-843-221A-165

; Sequence 165, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

; NUMBER OF SEQ ID NOS: 170

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 165

; LENGTH: 31

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Preferred embodiments - PTH

; NAME/KEY: misc_feature

; LOCATION: (31)..(31)

; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus

US-09-843-221A-165

Query Match 52.9%; Score 18; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 19

US-10-031-874A-206

; Sequence 206, Application US/10031874A

; Publication No. US20030190598A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANHA, JAMSHID
 ; APPLICANT: DUBUC, GINETTE
 ; APPLICANT: NARANG, SARAN
 ; TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS
 ; TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES
 ; FILE REFERENCE: 11054-1
 ; CURRENT APPLICATION NUMBER: US/10/031,874A
 ; CURRENT FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/207,234
 ; PRIOR FILING DATE: 2000-05-26
 ; NUMBER OF SEQ ID NOS: 212
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 206
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Lama glama
 US-10-031-874A-206

Query Match 52.9%; Score 18; DB 12; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
 |||||
 Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 20

US-10-361-928-9
 ; Sequence 9, Application US/10361928
 ; Publication No. US20030144209A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BRINGHURST, F. RICHARD
 ; APPLICANT: TAKASU, HISASHI
 ; APPLICANT: GARDELLA, THOMAS J.
 ; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
 ; TITLE OF INVENTION: ANALOGS
 ; FILE REFERENCE: 0609.4630002
 ; CURRENT APPLICATION NUMBER: US/10/361,928
 ; CURRENT FILING DATE: 2003-02-11
 ; PRIOR APPLICATION NUMBER: 09/447,800
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: 60/110,152
 ; PRIOR FILING DATE: 1998-11-25
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 33
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (1)
 ; OTHER INFORMATION: Desamino Ser
 US-10-361-928-9

Query Match 52.9%; Score 18; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
| | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 21

US-09-169-786-3
; Sequence 3, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-3

Query Match 52.9%; Score 18; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
| | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 22

US-09-928-047B-6
; Sequence 6, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-928-047B-6

Query Match 52.9%; Score 18; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 23

US-09-843-221A-16

; Sequence 16, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-16

Query Match 52.9%; Score 18; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 24

US-09-843-221A-88

; Sequence 88, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-88

Query Match 52.9%; Score 18; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSM 18
|||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 25

US-09-843-221A-89

; Sequence 89, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-89

Query Match 52.9%; Score 18; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
| | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 26

US-09-843-221A-90

; Sequence 90, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-90

Query Match 52.9%; Score 18; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
| | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 27

US-09-843-221A-91

; Sequence 91, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:

```

; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-91

```

```

Query Match          52.9%; Score 18; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSM 18
        |||||
Db      1 SVSEIQLMHNLGKHLNSM 18

```

RESULT 28

```

US-09-843-221A-92
; Sequence 92, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92

```

; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-92

Query Match 52.9%; Score 18; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 29

US-09-843-221A-128

; Sequence 128, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-128

Query Match 52.9%; Score 18; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 30

US-09-843-221A-161

```

; Sequence 161, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-161

```

```

Query Match          52.9%; Score 18; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSM 18
        |||||
Db      1 SVSEIQLMHNLGKHLNSM 18

```

RESULT 31

```

US-09-928-048A-6
; Sequence 6, Application US/09928048A
; Publication No. US20030138858A1
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT

```

; ORGANISM: Homo sapiens
US-09-928-048A-6

Query Match 52.9%; Score 18; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 32

US-10-361-928-8

; Sequence 8, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-10-361-928-8

Query Match 52.9%; Score 18; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 33

US-10-340-484-15

; Sequence 15, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic

; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-340-484-15

Query Match 52.9%; Score 18; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
| | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 34

US-10-340-484-16
; Sequence 16, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skeletal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-340-484-16

Query Match 52.9%; Score 18; DB 12; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
| | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 35

US-10-016-403-5

; Sequence 5, Application US/10016403
; Publication No. US20020107505A1

; GENERAL INFORMATION:

; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06

; ATTORNEY/AGENT INFORMATION:

; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "parathyroid hormone"

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-016-403-5

Query Match 52.9%; Score 18; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 36

US-10-016-403-7

; Sequence 7, Application US/10016403

; Publication No. US20020107505A1

; GENERAL INFORMATION:

; APPLICANT: Holladay, Leslie A.

; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard

; STREET: 25 West Main Street

; CITY: Madison

; STATE: WI

; COUNTRY: USA

; ZIP: 53701-2236

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/016,403

; FILING DATE: 10-Dec-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/466,610

; FILING DATE: 1995-JUN-06

; ATTORNEY/AGENT INFORMATION:

; NAME: Frenchick, Grady J.

; REGISTRATION NUMBER: 29,018

; REFERENCE/DOCKET NUMBER: 8734.28

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 608-257-2281

; TELEFAX: 608-257-7643

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..34

; OTHER INFORMATION: /note= "modified parathyroid
; hormone"

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-016-403-7

Query Match 52.9%; Score 18; DB 14; Length 34;

Best Local Similarity 100.0%; Pred. No. 1.1e-11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
| | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 37

US-10-097-079-1

; Sequence 1, Application US/10097079

; Publication No. US20020132973A1

; GENERAL INFORMATION:

; APPLICANT: Condon, Stephen M.

; Morize, Isabelle

; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS

; NUMBER OF SEQUENCES: 88

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rhone-Poulenc Rorer Inc.

; STREET: 500 Arcola Road, Mailstop 3C43

; CITY: Collegeville

; STATE: PA

; COUNTRY: USA

; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/097,079

; FILING DATE: 13-Mar-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/228,990

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 60/046,472

; FILING DATE: 14-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Martin Esq., Michael B.

; REGISTRATION NUMBER: 37,521

; REFERENCE/DOCKET NUMBER: A2678B-WO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (610) 454-2793

; TELEFAX: (610) 454-3808

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: No. US20020132973A1 Relevant

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-097-079-1

Query Match 52.9%; Score 18; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 38

US-10-168-185-9

; Sequence 9, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-9

Query Match 52.9%; Score 18; DB 12; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||||||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 39

US-09-169-786-4

; Sequence 4, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4

; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-4

Query Match 52.9%; Score 18; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||
Db 1 SVSEIQLMHNLGKHLNSM 18

RESULT 40

US-09-843-221A-14

; Sequence 14, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-14

Query Match 52.9%; Score 18; DB 11; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSM 18
|||
Db 1 SVSEIQLMHNLGKHLNSM 18

Search completed: January 14, 2004, 11:15:06
Job time : 24.8785 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 25.4206 Seconds
(without alignments)
345.145 Million cell updates/sec

Title: US-09-843-221A-164
Perfect score: 34
Sequence: 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 13497

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

1	14	41.2	31	11	Q91Y90	Q91y90 peromyscus
2	14	41.2	31	11	Q91Y91	Q91y91 peromyscus
3	5	14.7	34	5	O17148	O17148 echinococcu
4	5	14.7	34	16	Q97K50	Q97k50 clostridium
5	5	14.7	34	17	Q9HR65	Q9hr65 halobacteri
6	5	14.7	35	11	Q8BTB9	Q8btb9 mus musculu
7	5	14.7	35	16	Q97RG6	Q97rg6 streptococc
8	4	11.8	28	5	Q9BJE4	Q9bje4 pauropus sp
9	4	11.8	28	10	O24285	O24285 pinus radia
10	4	11.8	28	10	Q8GZQ8	Q8gzz8 hordeum vul
11	4	11.8	29	2	Q49148	Q49148 methylobact
12	4	11.8	29	4	Q9UCL2	Q9ucl2 homo sapien
13	4	11.8	29	4	Q96PP3	Q96pp3 homo sapien
14	4	11.8	29	5	Q25603	Q25603 onchocerca
15	4	11.8	29	8	Q9TI61	Q9ti61 allosyncarp
16	4	11.8	29	13	O13043	O13043 scyliorhinu
17	4	11.8	30	2	Q9REI5	Q9rei5 acidiphiliu
18	4	11.8	30	2	Q9JMV3	Q9jmv3 escherichia
19	4	11.8	30	4	Q9UBV5	Q9ubv5 homo sapien
20	4	11.8	30	16	Q8DZP7	Q8dzp7 streptococc
21	4	11.8	31	1	Q55314	Q55314 sulfolobus
22	4	11.8	31	4	Q8NEI8	Q8nei8 homo sapien
23	4	11.8	31	8	Q9MS77	Q9ms77 phacus acum
24	4	11.8	31	13	Q9PSU1	Q9psu1 xenopus lae
25	4	11.8	31	13	Q91816	Q91816 xenopus lae
26	4	11.8	31	16	O50669	O50669 borrelia bu
27	4	11.8	32	2	Q00491	Q00491 streptomyce
28	4	11.8	32	2	Q8KYN3	Q8kyn3 bacillus an
29	4	11.8	32	11	Q9QZQ2	Q9qzz2 mus musculu
30	4	11.8	32	17	Q9HSZ0	Q9hsz0 halobacteri
31	4	11.8	33	5	Q95SD4	Q95sd4 drosophila
32	4	11.8	33	16	Q9PKX3	Q9pkx3 chlamydia m
33	4	11.8	34	2	Q9ZG81	Q9zgz81 chlamydia t
34	4	11.8	34	2	Q8GFK2	Q8gfk2 staphylococ
35	4	11.8	34	11	Q8C4P4	Q8c4p4 mus musculu
36	4	11.8	34	13	Q90ZJ4	Q90zz4 gallus gall
37	4	11.8	34	16	Q98FK5	Q98fk5 rhizobium l
38	4	11.8	34	16	Q97FN0	Q97fn0 clostridium
39	4	11.8	34	16	Q8G2Q2	Q8g2q2 brucella su
40	4	11.8	35	4	Q15421	Q15421 homo sapien
41	4	11.8	35	12	Q8V6J8	Q8v6j8 halovirus h
42	4	11.8	35	16	Q9KQG4	Q9kqg4 vibrio chol
43	4	11.8	35	16	Q8F102	Q8f102 leptospira
44	4	11.8	36	2	O68941	O68941 rhodospiril
45	4	11.8	36	4	Q8WXW8	Q8wxw8 homo sapien
46	4	11.8	36	10	Q9SJ63	Q9sj63 arabidopsis
47	4	11.8	36	12	Q9PXD1	Q9pxd1 hepatitis c
48	4	11.8	36	12	Q91D77	Q91d77 ttv-like mi
49	4	11.8	36	16	Q97S91	Q97s91 streptococc
50	4	11.8	37	2	Q8KYJ0	Q8kyj0 bacillus an
51	4	11.8	37	10	Q39942	Q39942 helianthus
52	4	11.8	37	13	Q8AWW8	Q8aww8 oncorhynchu
53	4	11.8	37	16	Q8F6U2	Q8f6u2 leptospira
54	4	11.8	37	16	Q8F5H3	Q8f5h3 leptospira
55	4	11.8	37	16	Q8F419	Q8f419 leptospira
56	4	11.8	37	16	Q8EXV9	Q8exv9 leptospira
57	4	11.8	38	2	Q8KWH7	Q8kwh7 lactobacill

58	4	11.8	38	5	Q9NBE3	Q9nbe3 chironomus
59	4	11.8	38	5	O96619	O96619 echinococcu
60	4	11.8	38	5	Q9NBE5	Q9nbe5 chironomus
61	4	11.8	38	5	Q9NBE8	Q9nbe8 chironomus
62	4	11.8	38	5	Q9NBE4	Q9nbe4 chironomus
63	4	11.8	38	5	Q9NBE7	Q9nbe7 chironomus
64	4	11.8	38	11	Q91VC8	Q91vc8 mus musculu
65	4	11.8	38	13	Q8AWW9	Q8aww9 oncorhynchu
66	4	11.8	38	16	Q8E0D2	Q8e0d2 streptococc
67	4	11.8	39	2	Q8GPQ8	Q8gpg8 pseudomonas
68	4	11.8	39	10	Q9FEY1	Q9fey1 heterocapsa
69	4	11.8	39	12	Q68847	Q68847 hepatitis c
70	4	11.8	39	12	Q68845	Q68845 hepatitis c
71	4	11.8	39	12	Q68846	Q68846 hepatitis c
72	4	11.8	39	13	Q90776	Q90776 gallus gall
73	4	11.8	39	16	Q9KYH4	Q9kyh4 streptomyce
74	4	11.8	39	16	Q8F0C7	Q8f0c7 leptospira
75	4	11.8	39	16	Q8EZ33	Q8ez33 leptospira
76	4	11.8	40	2	Q48642	Q48642 lactococcus
77	4	11.8	40	2	Q8GCS7	Q8gcs7 eubacterium
78	4	11.8	40	4	P78340	P78340 homo sapien
79	4	11.8	40	5	Q9Nfq7	Q9nfq7 pachymerium
80	4	11.8	40	6	Q29283	Q29283 sus scrofa
81	4	11.8	40	10	Q8H192	Q8h192 arabidopsis
82	4	11.8	40	12	Q91JZ7	Q91jz7 hepatitis c
83	4	11.8	40	12	Q8V647	Q8v647 rabies viru
84	3	8.8	28	2	Q01303	Q01303 treponema p
85	3	8.8	28	2	Q9REI4	Q9rei4 acidiphiliu
86	3	8.8	28	2	Q05574	Q05574 prochloroth
87	3	8.8	28	2	Q9ZB83	Q9zb83 vibrio angu
88	3	8.8	28	3	Q8TGT8	Q8tgt8 saccharomyc
89	3	8.8	28	4	Q96SD9	Q96sd9 homo sapien
90	3	8.8	28	4	Q16326	Q16326 homo sapien
91	3	8.8	28	4	Q96EU0	Q96eu0 homo sapien
92	3	8.8	28	4	O75980	O75980 homo sapien
93	3	8.8	28	4	O95737	O95737 homo sapien
94	3	8.8	28	5	Q8MPY2	Q8mpy2 caenorhabdi
95	3	8.8	28	5	Q9BM68	Q9bm68 glottidia p
96	3	8.8	28	6	O62821	O62821 bubalus bub
97	3	8.8	28	6	Q9XS89	Q9xs89 equus cabal
98	3	8.8	28	8	Q8WBC8	Q8wbc8 cucurbita e
99	3	8.8	28	8	Q9TIE9	Q9tie9 centella er
100	3	8.8	28	8	Q9TIE8	Q9tie8 centella as
101	3	8.8	28	8	Q9MR96	Q9mr96 crocodylus
102	3	8.8	28	8	Q9TIE6	Q9tie6 centella hi
103	3	8.8	28	8	Q9ZYS4	Q9zys4 leishmania
104	3	8.8	28	8	Q9MR94	Q9mr94 chelonias my
105	3	8.8	28	8	Q9TIE7	Q9tie7 centella tr
106	3	8.8	28	8	Q8HS23	Q8hs23 pisum sativ
107	3	8.8	28	8	Q8HS11	Q8hs11 spathiphyll
108	3	8.8	28	8	Q8HS07	Q8hs07 welwitschia
109	3	8.8	28	9	Q9AZJ9	Q9azj9 bacterioph
110	3	8.8	28	9	Q38269	Q38269 bacterioph
111	3	8.8	28	10	Q8S526	Q8s526 ipomoea bat
112	3	8.8	28	10	Q9LQI0	Q9lqi0 arabidopsis
113	3	8.8	28	10	Q8W232	Q8w232 zeamays (m
114	3	8.8	28	10	Q9LMD6	Q9lmd6 arabidopsis

115	3	8.8	28	10	Q944P1	Q944p1 manihot esc
116	3	8.8	28	11	Q9ESI4	Q9esi4 petromus ty
117	3	8.8	28	11	Q9ESI5	Q9esi5 thryonomys
118	3	8.8	28	11	Q9ESI6	Q9esi6 hystrix afr
119	3	8.8	28	11	Q99PL9	Q99pl9 mus musculu
120	3	8.8	28	11	Q9ESI2	Q9esi2 cryptomys h
121	3	8.8	28	11	Q9EP60	Q9ep60 heliophobi
122	3	8.8	28	11	Q9ESI0	Q9esi0 cryptomys s
123	3	8.8	28	11	Q91XP0	Q91xp0 rattus norv
124	3	8.8	28	11	P70651	P70651 mus sp. bet
125	3	8.8	28	11	Q9EP59	Q9ep59 georychus c
126	3	8.8	28	11	Q9ESI1	Q9esi1 cryptomys d
127	3	8.8	28	11	P97914	P97914 rattus norv
128	3	8.8	28	11	Q9EP61	Q9ep61 heteroceph
129	3	8.8	28	11	Q9ESH8	Q9esh8 bathyergus
130	3	8.8	28	11	Q9ESH9	Q9esh9 bathyergus
131	3	8.8	28	11	Q9QXB4	Q9qxb4 mus musculu
132	3	8.8	28	11	Q9ESI3	Q9esi3 cryptomys h
133	3	8.8	28	12	Q68087	Q68087 hepatitis c
134	3	8.8	28	12	Q68095	Q68095 hepatitis c
135	3	8.8	28	12	Q68097	Q68097 hepatitis c
136	3	8.8	28	12	Q68092	Q68092 hepatitis c
137	3	8.8	28	12	Q68091	Q68091 hepatitis c
138	3	8.8	28	12	Q68093	Q68093 hepatitis c
139	3	8.8	28	12	Q68099	Q68099 hepatitis c
140	3	8.8	28	12	Q68096	Q68096 hepatitis c
141	3	8.8	28	12	Q68098	Q68098 hepatitis c
142	3	8.8	28	12	Q83181	Q83181 cauliflower
143	3	8.8	28	12	Q68086	Q68086 hepatitis c
144	3	8.8	28	12	Q68552	Q68552 hepatitis c
145	3	8.8	28	12	Q68094	Q68094 hepatitis c
146	3	8.8	28	12	Q9WNI4	Q9wni4 tt virus. o
147	3	8.8	28	13	Q9PRT6	Q9prt6 rana catesb
148	3	8.8	28	13	Q9PRE8	Q9pre8 oryzias lat
149	3	8.8	28	13	Q9PRI9	Q9pri9 amia calva
150	3	8.8	28	13	Q9PRN8	Q9prn8 carassius a
151	3	8.8	28	15	Q75721	Q75721 human immun
152	3	8.8	28	15	O71346	O71346 human endog
153	3	8.8	28	15	Q75720	Q75720 human immun
154	3	8.8	28	15	Q9QEY3	Q9qey3 human immun
155	3	8.8	28	16	Q8X415	Q8x415 escherichia
156	3	8.8	28	16	Q8ENT7	Q8ent7 oceanobacil
157	3	8.8	28	16	Q8CK95	Q8ck95 yersinia pe
158	3	8.8	29	2	Q9ZGG4	Q9zgg4 heliobacill
159	3	8.8	29	2	Q9X3E3	Q9x3e3 prochloroco
160	3	8.8	29	2	Q9X3J9	Q9x3j9 prochloroco
161	3	8.8	29	2	Q47650	Q47650 escherichia
162	3	8.8	29	2	Q9AKV1	Q9akv1 neisseria g
163	3	8.8	29	2	Q9R526	Q9r526 vibrio chol
164	3	8.8	29	3	P78747	P78747 saccharomyc
165	3	8.8	29	3	Q8TGQ5	Q8tgq5 saccharomyc
166	3	8.8	29	4	Q9Y3G1	Q9y3g1 homo sapien
167	3	8.8	29	4	Q9H2A1	Q9h2a1 homo sapien
168	3	8.8	29	4	Q9H465	Q9h465 homo sapien
169	3	8.8	29	4	Q8NEF6	Q8nef6 homo sapien
170	3	8.8	29	4	Q8TDW8	Q8tdw8 homo sapien
171	3	8.8	29	4	Q96IR5	Q96ir5 homo sapien

172	3	8.8	29	4	Q9BSQ3	Q9bsq3	homo sapien
173	3	8.8	29	5	Q95VB2	Q95vb2	spirometra
174	3	8.8	29	5	Q95NF4	Q95nf4	drosophila
175	3	8.8	29	5	Q24683	Q24683	dugesia tig
176	3	8.8	29	5	Q8T936	Q8t936	folsomia ca
177	3	8.8	29	6	Q9TRG5	Q9trg5	sus scrofa
178	3	8.8	29	8	Q8WBB9	Q8wbb9	cucurbita f
179	3	8.8	29	8	Q9TI57	Q9ti57	corymbia pa
180	3	8.8	29	8	Q8W7W7	Q8w7w7	cucurbita p
181	3	8.8	29	8	Q9GF70	Q9gf70	trochodendr
182	3	8.8	29	8	Q8W7W4	Q8w7w4	cucurbita a
183	3	8.8	29	8	Q8W7W6	Q8w7w6	cucurbita p
184	3	8.8	29	8	Q8WBC1	Q8wbc1	cucurbita o
185	3	8.8	29	8	Q9B5Z6	Q9b5z6	pseudostylo
186	3	8.8	29	8	Q8W7W5	Q8w7w5	cucurbita p
187	3	8.8	29	8	Q9B938	Q9b938	eupristina
188	3	8.8	29	8	Q9G370	Q9g370	draco blanf
189	3	8.8	29	8	Q8WBD0	Q8wbd0	cucurbita a
190	3	8.8	29	8	Q8WBB6	Q8wbb6	citrullus l
191	3	8.8	29	8	Q8W7W9	Q8w7w9	cucurbita f
192	3	8.8	29	8	Q8W7W8	Q8w7w8	cucurbita m
193	3	8.8	29	8	Q8HS21	Q8hs21	rheum x cul
194	3	8.8	29	9	Q9FZX6	Q9fzx6	bacterioph
195	3	8.8	29	10	P82196	P82196	spinacia ol
196	3	8.8	29	11	Q9Z2C0	Q9z2c0	mus musculu
197	3	8.8	29	11	Q921Z6	Q921z6	mus musculu
198	3	8.8	29	11	Q9Z2C1	Q9z2c1	mus musculu
199	3	8.8	29	11	O70564	O70564	mus musculu
200	3	8.8	29	11	Q62777	Q62777	rattus norv
201	3	8.8	29	11	O08980	O08980	mus musculu
202	3	8.8	29	11	Q8CGM8	Q8cgm8	mus musculu
203	3	8.8	29	12	Q91HB1	Q91hb1	porcine cir
204	3	8.8	29	12	O92646	O92646	hepatitis e
205	3	8.8	29	12	Q919A5	Q919a5	porcine rep
206	3	8.8	29	12	Q919A7	Q919a7	porcine rep
207	3	8.8	29	12	Q86872	Q86872	cauliflower
208	3	8.8	29	12	O92648	O92648	hepatitis e
209	3	8.8	29	12	O56835	O56835	vibrio chol
210	3	8.8	29	13	P82235	P82235	rana tempor
211	3	8.8	29	13	Q8AYR0	Q8ayr0	oryzias lat
212	3	8.8	29	13	Q8AWC2	Q8awc2	gallus gall
213	3	8.8	29	15	O72001	O72001	human endog
214	3	8.8	29	15	O71342	O71342	human endog
215	3	8.8	29	15	O71339	O71339	human endog
216	3	8.8	29	15	O71347	O71347	human endog
217	3	8.8	29	15	O71340	O71340	human endog
218	3	8.8	29	15	P89816	P89816	human immun
219	3	8.8	29	15	O71343	O71343	human endog
220	3	8.8	29	15	O71991	O71991	human endog
221	3	8.8	29	15	O71994	O71994	human endog
222	3	8.8	29	15	O71341	O71341	human endog
223	3	8.8	29	15	O71345	O71345	human endog
224	3	8.8	29	15	P89821	P89821	human immun
225	3	8.8	29	15	O71336	O71336	human endog
226	3	8.8	29	15	O71344	O71344	human endog
227	3	8.8	29	15	O71338	O71338	human endog
228	3	8.8	29	15	O71992	O71992	human endog

229	3	8.8	29	15	071337	071337 human endog
230	3	8.8	29	15	071997	071997 human endog
231	3	8.8	29	15	071335	071335 human endog
232	3	8.8	29	16	Q9JZN6	Q9jzn6 neisseria m
233	3	8.8	29	16	Q8X419	Q8x419 escherichia
234	3	8.8	29	17	Q8Q0H5	Q8q0h5 methanosarc
235	3	8.8	30	2	Q9JP75	Q9jp75 salmonella
236	3	8.8	30	2	Q9L8W9	Q9l8w9 streptomyce
237	3	8.8	30	2	Q9L8X1	Q9l8x1 streptomyce
238	3	8.8	30	2	Q9R4Z6	Q9r4z6 clostridium
239	3	8.8	30	2	Q9R4J2	Q9r4j2 helicobacte
240	3	8.8	30	2	Q8VUW9	Q8vuw9 staphylococ
241	3	8.8	30	2	Q9R4I5	Q9r4i5 mycoplasma
242	3	8.8	30	2	Q9R5Q3	Q9r5q3 leuconostoc
243	3	8.8	30	2	Q93GF6	Q93gf6 staphylococ
244	3	8.8	30	2	Q9R5K3	Q9r5k3 leptospira
245	3	8.8	30	2	Q9R4I6	Q9r4i6 mycoplasma
246	3	8.8	30	2	Q9RER6	Q9rer6 enterobacte
247	3	8.8	30	2	Q8GF47	Q8gf47 zymomonas m
248	3	8.8	30	3	Q8TGM3	Q8tgm3 saccharomyc
249	3	8.8	30	3	Q9URB0	Q9urb0 candida alb
250	3	8.8	30	3	Q8J172	Q8j172 trichoderma
251	3	8.8	30	3	Q8J171	Q8j171 hypocrea li
252	3	8.8	30	4	Q16330	Q16330 homo sapien
253	3	8.8	30	4	O95595	O95595 homo sapien
254	3	8.8	30	4	P78460	P78460 homo sapien
255	3	8.8	30	4	Q8N563	Q8n563 homo sapien
256	3	8.8	30	4	P78542	P78542 homo sapien
257	3	8.8	30	4	Q8IU66	Q8iu66 homo sapien
258	3	8.8	30	5	Q8SZJ6	Q8szj6 drosophila
259	3	8.8	30	5	Q9TWH7	Q9twh7 ancylostoma
260	3	8.8	30	5	Q968N1	Q968n1 tritrichomo
261	3	8.8	30	5	P82214	P82214 bombyx mori
262	3	8.8	30	5	Q8I868	Q8i868 acanthamoeb
263	3	8.8	30	6	Q9BDK1	Q9bdk1 bos taurus
264	3	8.8	30	8	Q8W7L1	Q8w7l1 cucurbita m
265	3	8.8	30	8	Q8W7K9	Q8w7k9 cucurbita p
266	3	8.8	30	8	Q8W7H8	Q8w7h8 cucurbita a
267	3	8.8	30	8	Q8WBC2	Q8wbc2 cucurbita o
268	3	8.8	30	8	Q8W7K8	Q8w7k8 cucurbita p
269	3	8.8	30	8	Q8W7H6	Q8w7h6 cucurbita m
270	3	8.8	30	8	Q8WBC4	Q8wbc4 cucurbita p
271	3	8.8	30	8	Q8W7L2	Q8w7l2 cucurbita a
272	3	8.8	30	8	Q8WBC6	Q8wbc6 cucurbita a
273	3	8.8	30	8	Q8WBB7	Q8wbb7 sechium edu
274	3	8.8	30	8	Q99328	Q99328 meloidogyne
275	3	8.8	30	8	Q8W7H7	Q8w7h7 cucurbita e
276	3	8.8	30	8	Q8WBC0	Q8wbc0 cucurbita f
277	3	8.8	30	8	Q9T2T8	Q9t2t8 bos taurus
278	3	8.8	30	8	Q8W7L0	Q8w7l0 cucurbita p
279	3	8.8	30	8	Q9TI56	Q9ti56 eucalyptus
280	3	8.8	30	9	Q8W674	Q8w674 enterobacte
281	3	8.8	30	10	Q9S8T2	Q9s8t2 cicer ariet
282	3	8.8	30	10	O23933	O23933 flaveria tr
283	3	8.8	30	10	Q8RUD1	Q8rud1 zea mays (m
284	3	8.8	30	10	Q93WY2	Q93wy2 oryza sativ
285	3	8.8	30	11	Q63885	Q63885 mus sp. cys

286	3	8.8	30	11	O88549	O88549 mesocricetu
287	3	8.8	30	11	Q8VDL1	Q8vdl1 mus musculu
288	3	8.8	30	11	Q9QV18	Q9qv18 rattus sp.
289	3	8.8	30	11	Q9QV14	Q9qv14 mus sp. col
290	3	8.8	30	11	Q9QV19	Q9qv19 rattus sp.
291	3	8.8	30	11	Q10753	Q10753 rattus norv
292	3	8.8	30	11	Q8BR32	Q8br32 mus musculu
293	3	8.8	30	12	Q91HB7	Q91hb7 tt virus. o
294	3	8.8	30	12	Q91HC4	Q91hc4 tt virus. o
295	3	8.8	30	12	Q9IJV5	Q9ijv5 norwalk vir
296	3	8.8	30	12	Q86870	Q86870 cauliflower
297	3	8.8	30	12	Q91HC3	Q91hc3 tt virus. o
298	3	8.8	30	12	Q9WLK3	Q9wlk3 hepatitis e
299	3	8.8	30	12	Q91HC0	Q91hc0 tt virus. o
300	3	8.8	30	13	O42551	O42551 brachydanio
301	3	8.8	30	13	Q9PRW0	Q9prw0 struthio ca
302	3	8.8	30	13	Q9PT00	Q9pt00 oncorhynch
303	3	8.8	30	15	Q86599	Q86599 human endog
304	3	8.8	30	15	Q991P5	Q991p5 human immun
305	3	8.8	30	16	O50822	O50822 borrelia bu
306	3	8.8	30	16	Q9X0W9	Q9x0w9 thermotoga
307	3	8.8	30	16	Q9PP53	Q9pp53 campylobact
308	3	8.8	30	16	Q9KU55	Q9ku55 vibrio chol
309	3	8.8	30	16	Q9KT75	Q9kt75 vibrio chol
310	3	8.8	30	16	Q9JWF4	Q9jwf4 neisseria m
311	3	8.8	30	16	Q97SY9	Q97sy9 streptococc
312	3	8.8	30	16	Q97SX5	Q97sx5 streptococc
313	3	8.8	30	16	Q9K1W7	Q9k1w7 chlamydia p
314	3	8.8	30	16	Q8KE55	Q8ke55 chlorobium
315	3	8.8	30	16	Q93RS7	Q93rs7 streptomyce
316	3	8.8	30	16	Q8G1R1	Q8glr1 brucella su
317	3	8.8	30	16	Q8FZX9	Q8fzx9 brucella su
318	3	8.8	30	16	Q8CU88	Q8cu88 staphylococ
319	3	8.8	30	17	Q8ZZF0	Q8zzf0 pyrobaculum
320	3	8.8	30	17	Q8ZVL0	Q8zvl0 pyrobaculum
321	3	8.8	31	2	Q54825	Q54825 streptococc
322	3	8.8	31	2	Q9S619	Q9s619 prochloroco
323	3	8.8	31	2	Q8KYK0	Q8kyk0 bacillus an
324	3	8.8	31	2	Q9JMV2	Q9jmv2 escherichia
325	3	8.8	31	2	Q9X3C3	Q9x3c3 prochloroco
326	3	8.8	31	2	O68825	O68825 pseudomonas
327	3	8.8	31	2	Q9KH08	Q9kh08 thermus aqu
328	3	8.8	31	2	Q93GF7	Q93gf7 staphylococ
329	3	8.8	31	2	Q47323	Q47323 escherichia
330	3	8.8	31	2	Q9RHF9	Q9rhf9 acinetobact
331	3	8.8	31	2	Q9R4X1	Q9r4x1 treponema d
332	3	8.8	31	2	Q8KYI9	Q8kyi9 bacillus an
333	3	8.8	31	2	Q8RTS5	Q8rts5 uncultured
334	3	8.8	31	2	Q8L3D3	Q8l3d3 colwellia m
335	3	8.8	31	2	Q93PE1	Q93pel yersinia ps
336	3	8.8	31	3	O94120	O94120 saccharomyc
337	3	8.8	31	4	Q96A45	Q96a45 homo sapien
338	3	8.8	31	4	Q9UHM9	Q9uhm9 homo sapien
339	3	8.8	31	4	Q9UEA9	Q9uea9 homo sapien
340	3	8.8	31	4	Q8WYF5	Q8wyf5 homo sapien
341	3	8.8	31	4	Q8N5X3	Q8n5x3 homo sapien
342	3	8.8	31	4	Q9BXM4	Q9bxm4 homo sapien

343	3	8.8	31	4	Q9UDE5	Q9ude5	homo sapien
344	3	8.8	31	5	Q8IQV3	Q8iqv3	drosophila
345	3	8.8	31	5	Q8IF28	Q8if28	trypanosoma
346	3	8.8	31	5	Q8IEY3	Q8iey3	trypanosoma
347	3	8.8	31	6	Q8MI94	Q8mi94	tupaia tana
348	3	8.8	31	6	Q9GLD6	Q9gld6	sus scrofa
349	3	8.8	31	6	Q8MIH5	Q8mih5	canis famil
350	3	8.8	31	6	Q8MIC3	Q8mic3	ochotona pr
351	3	8.8	31	6	Q95LC0	Q95lc0	sus scrofa
352	3	8.8	31	6	Q9N1C8	Q9nlc8	ovis aries
353	3	8.8	31	6	Q8MIC9	Q8mic9	nycticebus
354	3	8.8	31	6	Q9GKL4	Q9gkl4	canis famil
355	3	8.8	31	6	Q8MIG4	Q8mig4	cynocephalu
356	3	8.8	31	6	Q9XSB9	Q9xsb9	ateles belz
357	3	8.8	31	7	Q29868	Q29868	homo sapien
358	3	8.8	31	8	Q9MNM2	Q9mnm2	bufo americ
359	3	8.8	31	8	Q9MS59	Q9ms59	euglena san
360	3	8.8	31	8	O80011	O80011	enallagma a
361	3	8.8	31	8	Q9MS62	Q9ms62	euglena myx
362	3	8.8	31	8	Q34922	Q34922	limulus pol
363	3	8.8	31	8	Q8WEJ4	Q8wej4	gnetum gnem
364	3	8.8	31	8	Q9MS74	Q9ms74	euglena ana
365	3	8.8	31	8	Q9MS68	Q9ms68	euglena des
366	3	8.8	31	8	Q8M9Y3	Q8m9y3	chaetosphae
367	3	8.8	31	8	Q9MS53	Q9ms53	euglena vir
368	3	8.8	31	8	Q9MNL2	Q9mnl2	torrentophr
369	3	8.8	31	8	Q9MS56	Q9ms56	euglena ste
370	3	8.8	31	8	Q9MS78	Q9ms78	phacus acum
371	3	8.8	31	8	Q9MNL3	Q9mnl3	torrentophr
372	3	8.8	31	9	Q38499	Q38499	bacteriopha
373	3	8.8	31	9	O64265	O64265	mycobacteri
374	3	8.8	31	10	Q9XIT0	Q9xit0	glycine max
375	3	8.8	31	10	Q8LKB4	Q8lkb4	musa acumin
376	3	8.8	31	11	Q8K1W2	Q8klw2	cavia porce
377	3	8.8	31	11	Q9QXB6	Q9qxb6	mus musculu
378	3	8.8	31	11	Q99KK6	Q99kk6	mus musculu
379	3	8.8	31	11	Q8K1P4	Q8klp4	sciurus vul
380	3	8.8	31	11	Q8CGM7	Q8cgm7	mus musculu
381	3	8.8	31	12	Q919E5	Q919e5	human papil
382	3	8.8	31	12	Q919E4	Q919e4	human papil
383	3	8.8	31	12	O56713	O56713	hepatitis c
384	3	8.8	31	12	Q919F7	Q919f7	human papil
385	3	8.8	31	12	Q919E6	Q919e6	human papil
386	3	8.8	31	12	O56692	O56692	hepatitis c
387	3	8.8	31	12	Q919F3	Q919f3	human papil
388	3	8.8	31	12	O56707	O56707	hepatitis c
389	3	8.8	31	12	O56687	O56687	hepatitis c
390	3	8.8	31	12	Q919F8	Q919f8	human papil
391	3	8.8	31	12	O56691	O56691	hepatitis c
392	3	8.8	31	12	Q919E1	Q919e1	human papil
393	3	8.8	31	12	O56701	O56701	hepatitis c
394	3	8.8	31	12	O56694	O56694	hepatitis c
395	3	8.8	31	12	Q919D9	Q919d9	human papil
396	3	8.8	31	12	Q919F6	Q919f6	human papil
397	3	8.8	31	12	Q919E3	Q919e3	human papil
398	3	8.8	31	12	O56712	O56712	hepatitis c
399	3	8.8	31	12	Q919E8	Q919e8	human papil

400	3	8.8	31	12	056710	056710 hepatitis c
401	3	8.8	31	12	056688	056688 hepatitis c
402	3	8.8	31	12	056696	056696 hepatitis c
403	3	8.8	31	12	056695	056695 hepatitis c
404	3	8.8	31	12	056698	056698 hepatitis c
405	3	8.8	31	12	056702	056702 hepatitis c
406	3	8.8	31	12	056703	056703 hepatitis c
407	3	8.8	31	12	056697	056697 hepatitis c
408	3	8.8	31	12	Q919F0	Q919f0 human papil
409	3	8.8	31	12	056709	056709 hepatitis c
410	3	8.8	31	12	Q919F4	Q919f4 human papil
411	3	8.8	31	12	056689	056689 hepatitis c
412	3	8.8	31	12	Q919F2	Q919f2 human papil
413	3	8.8	31	12	Q919F1	Q919f1 human papil
414	3	8.8	31	12	056711	056711 hepatitis c
415	3	8.8	31	12	Q919E2	Q919e2 human papil
416	3	8.8	31	12	Q919D8	Q919d8 human papil
417	3	8.8	31	12	056686	056686 hepatitis c
418	3	8.8	31	12	Q9WMX5	Q9wmx5 human echov
419	3	8.8	31	12	056690	056690 hepatitis c
420	3	8.8	31	12	Q919E9	Q919e9 human papil
421	3	8.8	31	12	056706	056706 hepatitis c
422	3	8.8	31	12	056700	056700 hepatitis c
423	3	8.8	31	12	056704	056704 hepatitis c
424	3	8.8	31	12	Q919D7	Q919d7 human papil
425	3	8.8	31	12	Q919F5	Q919f5 human papil
426	3	8.8	31	12	056693	056693 hepatitis c
427	3	8.8	31	12	056685	056685 hepatitis c
428	3	8.8	31	12	056708	056708 hepatitis c
429	3	8.8	31	12	Q919E0	Q919e0 human papil
430	3	8.8	31	12	056705	056705 hepatitis c
431	3	8.8	31	12	Q919E7	Q919e7 human papil
432	3	8.8	31	12	Q914M9	Q914m9 sulfolobus
433	3	8.8	31	12	056699	056699 hepatitis c
434	3	8.8	31	13	042540	042540 brachydanio
435	3	8.8	31	13	Q91763	Q91763 xenopus lae
436	3	8.8	31	15	Q83937	Q83937 ovine lenti
437	3	8.8	31	16	025108	025108 helicobacte
438	3	8.8	31	16	050709	050709 borrelia bu
439	3	8.8	31	16	050818	050818 borrelia bu
440	3	8.8	31	16	050858	050858 borrelia bu
441	3	8.8	31	16	051007	051007 borrelia bu
442	3	8.8	31	16	Q9PGF2	Q9pgf2 xylella fas
443	3	8.8	31	16	Q9PAW4	Q9paw4 xylella fas
444	3	8.8	31	16	Q9KVF3	Q9kvf3 vibrio chol
445	3	8.8	31	16	Q9K7A8	Q9k7a8 bacillus ha
446	3	8.8	31	16	Q9JXQ7	Q9jxq7 neisseria m
447	3	8.8	31	16	Q97SZ9	Q97sz9 streptococc
448	3	8.8	31	16	Q97QJ4	Q97qj4 streptococc
449	3	8.8	31	16	Q97QB7	Q97qb7 streptococc
450	3	8.8	31	16	Q97CV6	Q97cv6 streptococc
451	3	8.8	31	16	Q9K2A0	Q9k2a0 chlamydia p
452	3	8.8	31	16	Q9K236	Q9k236 chlamydia p
453	3	8.8	31	16	Q8VJ13	Q8vj13 mycobacteri
454	3	8.8	31	16	Q8VWC7	Q8vwc7 streptomyce
455	3	8.8	31	16	Q9ZK13	Q9zk13 helicobacte
456	3	8.8	31	16	Q8P9W1	Q8p9w1 xanthomonas

457	3	8.8	31	16	Q8KEV8	Q8kev8 chlorobium
458	3	8.8	31	16	Q8KCQ0	Q8kcq0 chlorobium
459	3	8.8	31	16	Q8KBJ8	Q8kbj8 chlorobium
460	3	8.8	31	16	Q8EIW8	Q8eiw8 shewanella
461	3	8.8	31	16	Q8EI77	Q8ei77 shewanella
462	3	8.8	31	16	Q8E9Y5	Q8e9y5 shewanella
463	3	8.8	31	16	Q8E8G1	Q8e8g1 shewanella
464	3	8.8	31	16	Q8CTW3	Q8ctw3 staphylococ
465	3	8.8	31	16	Q8CTA2	Q8cta2 staphylococ
466	3	8.8	32	2	Q9AJ41	Q9aj41 buchnera ap
467	3	8.8	32	2	Q49249	Q49249 mycoplasma
468	3	8.8	32	2	Q44499	Q44499 anabaena va
469	3	8.8	32	2	Q9S629	Q9s629 prochloroco
470	3	8.8	32	2	Q44509	Q44509 azotobacter
471	3	8.8	32	2	Q45534	Q45534 bacillus su
472	3	8.8	32	2	Q9R5Q7	Q9r5q7 aeromonas h
473	3	8.8	32	2	Q8KYM4	Q8kym4 bacillus an
474	3	8.8	32	2	O32493	O32493 bacteroides
475	3	8.8	32	2	Q9L373	Q9l373 rhizobium l
476	3	8.8	32	2	Q8GF58	Q8gf58 zymomonas m
477	3	8.8	32	3	Q01058	Q01058 kluyveromyc
478	3	8.8	32	3	Q8TGT3	Q8tgt3 saccharomyc
479	3	8.8	32	4	Q9UEB0	Q9ueb0 homo sapien
480	3	8.8	32	4	Q8TC25	Q8tc25 homo sapien
481	3	8.8	32	4	Q9BPX8	Q9bpx8 homo sapien
482	3	8.8	32	4	Q96GM7	Q96gm7 homo sapien
483	3	8.8	32	4	Q9HAX8	Q9hax8 homo sapien
484	3	8.8	32	4	Q8TBQ3	Q8tbq3 homo sapien
485	3	8.8	32	4	Q96I20	Q96i20 homo sapien
486	3	8.8	32	4	Q9UN69	Q9un69 homo sapien
487	3	8.8	32	4	Q9UQV1	Q9uqv1 homo sapien
488	3	8.8	32	5	Q26651	Q26651 strongyloce
489	3	8.8	32	5	Q8T382	Q8t382 leishmania
490	3	8.8	32	5	O96634	O96634 trypanosoma
491	3	8.8	32	5	Q9TWR8	Q9twr8 procambarus
492	3	8.8	32	5	O18606	O18606 branchiosto
493	3	8.8	32	6	Q9TR67	Q9tr67 sus scrofa
494	3	8.8	32	6	Q9TR69	Q9tr69 sus scrofa
495	3	8.8	32	6	Q8MJ42	Q8mj42 equus cabal
496	3	8.8	32	6	Q9TSE6	Q9tse6 oryctolagus
497	3	8.8	32	6	Q8MJ91	Q8mj91 macaca mula
498	3	8.8	32	7	O19722	O19722 homo sapien
499	3	8.8	32	8	Q36494	Q36494 farfantepen
500	3	8.8	32	8	Q8SL89	Q8sl89 euglena ste
501	3	8.8	32	8	Q9GF95	Q9gf95 cercidiphyl
502	3	8.8	32	8	Q31736	Q31736 beta vulgar
503	3	8.8	32	8	Q8SL87	Q8sl87 euglena vir
504	3	8.8	32	8	Q31735	Q31735 beta vulgar
505	3	8.8	32	8	Q9MNM0	Q9mnm0 bufo andrew
506	3	8.8	32	8	Q9MNL0	Q9mnl0 bufo danate
507	3	8.8	32	8	Q951Q4	Q951q4 renilla ren
508	3	8.8	32	8	Q9GF72	Q9gf72 saururus ce
509	3	8.8	32	9	Q9MBU5	Q9mbu5 chlamydia p
510	3	8.8	32	10	Q8S527	Q8s527 ipomoea bat
511	3	8.8	32	10	Q40727	Q40727 oryza sativ
512	3	8.8	32	11	Q9JIU1	Q9jiu1 rattus norv
513	3	8.8	32	11	Q9R0E3	Q9r0e3 mus musculu

514	3	8.8	32	11	Q9QWM2	Q9qwm2	mus musculu
515	3	8.8	32	11	Q9QWB2	Q9qwb2	rattus sp.
516	3	8.8	32	11	Q9QXX1	Q9qxx1	mus musculu
517	3	8.8	32	11	Q8C2N8	Q8c2n8	mus musculu
518	3	8.8	32	11	Q8BS12	Q8bs12	mus musculu
519	3	8.8	32	12	Q9PXV2	Q9pxv2	hepatitis b
520	3	8.8	32	12	Q9WNI5	Q9wni5	tt virus. o
521	3	8.8	32	12	Q914F9	Q914f9	sulfolobus
522	3	8.8	32	12	Q8QYT4	Q8qyt4	grapevine v
523	3	8.8	32	12	Q8QYT7	Q8qyt7	grapevine v
524	3	8.8	32	12	Q8QYU0	Q8qyu0	grapevine v
525	3	8.8	32	12	Q9Q934	Q9q934	shope fibro
526	3	8.8	32	13	Q8QG73	Q8qg73	oncorhynchu
527	3	8.8	32	13	Q8QG72	Q8qg72	salmo salar
528	3	8.8	32	13	Q8QG71	Q8qg71	oncorhynchu
529	3	8.8	32	13	Q9PS21	Q9ps21	carassius a
530	3	8.8	32	13	Q8QG84	Q8qg84	oncorhynchu
531	3	8.8	32	13	Q8QG83	Q8qg83	oncorhynchu
532	3	8.8	32	13	Q8QG82	Q8qg82	oncorhynchu
533	3	8.8	32	13	Q8QG70	Q8qg70	salvelinus
534	3	8.8	32	13	P82780	P82780	rana catesb
535	3	8.8	32	13	Q9W7P3	Q9w7p3	morone saxa
536	3	8.8	32	13	Q9W7P2	Q9w7p2	morone saxa
537	3	8.8	32	16	O50706	O50706	borrelia bu
538	3	8.8	32	16	O50851	O50851	borrelia bu
539	3	8.8	32	16	O50865	O50865	borrelia bu
540	3	8.8	32	16	Q9PGT0	Q9pgt0	xylella fas
541	3	8.8	32	16	Q9KVF7	Q9kvf7	vibrio chol
542	3	8.8	32	16	Q9KTV2	Q9ktv2	vibrio chol
543	3	8.8	32	16	Q9KPN9	Q9kpn9	vibrio chol
544	3	8.8	32	16	Q9KLF0	Q9klf0	vibrio chol
545	3	8.8	32	16	Q9K7B0	Q9k7b0	bacillus ha
546	3	8.8	32	16	Q9A2H0	Q9a2h0	caulobacter
547	3	8.8	32	16	Q98AB6	Q98ab6	rhizobium l
548	3	8.8	32	16	Q97R92	Q97r92	streptococc
549	3	8.8	32	16	Q8X3V6	Q8x3v6	escherichia
550	3	8.8	32	16	Q8VKF9	Q8vkf9	mycobacteri
551	3	8.8	32	16	Q8KG49	Q8kg49	chlorobium
552	3	8.8	32	16	Q8KF24	Q8kf24	chlorobium
553	3	8.8	32	16	Q8KCV3	Q8kcv3	chlorobium
554	3	8.8	32	16	Q9K4G0	Q9k4g0	streptomyce
555	3	8.8	32	16	Q8EJ44	Q8ej44	shewanella
556	3	8.8	32	16	Q8EC15	Q8ec15	shewanella
557	3	8.8	32	16	Q8EAD5	Q8ead5	shewanella
558	3	8.8	32	16	Q8CU60	Q8cu60	staphylococ
559	3	8.8	32	16	Q8CTR7	Q8ctr7	staphylococ
560	3	8.8	32	16	Q8CRE7	Q8cre7	staphylococ
561	3	8.8	32	17	Q8ZZF7	Q8zzf7	pyrobaculum
562	3	8.8	33	1	Q9UWL4	Q9uwl4	methanopyru
563	3	8.8	33	2	Q8KH96	Q8kh96	pseudomonas
564	3	8.8	33	2	Q9S624	Q9s624	prochloroco
565	3	8.8	33	2	Q9R2M3	Q9r2m3	prochloroco
566	3	8.8	33	2	Q9X3M5	Q9x3m5	prochloroco
567	3	8.8	33	2	Q9S651	Q9s651	streptococc
568	3	8.8	33	2	Q9K533	Q9k533	listeria mo
569	3	8.8	33	2	Q9K370	Q9k370	rhizobium l
570	3	8.8	33	2	Q9F2C4	Q9f2c4	salmonella

571	3	8.8	33	2	Q9S3N5	Q9s3n5	bacillus ce
572	3	8.8	33	2	Q8KQ80	Q8kq80	vibrio chol
573	3	8.8	33	2	Q56414	Q56414	escherichia
574	3	8.8	33	2	Q9S622	Q9s622	prochloroco
575	3	8.8	33	2	Q9K2V1	Q9k2v1	rhizobium l
576	3	8.8	33	2	Q9F1F4	Q9flf4	enterococcu
577	3	8.8	33	2	Q9KI23	Q9ki23	helicobacte
578	3	8.8	33	2	Q8GQU2	Q8gqu2	leptospira
579	3	8.8	33	3	Q8TGR1	Q8tgr1	saccharomyc
580	3	8.8	33	4	Q99950	Q99950	homo sapien
581	3	8.8	33	4	Q8N363	Q8n363	homo sapien
582	3	8.8	33	4	Q9UP36	Q9up36	homo sapien
583	3	8.8	33	4	Q15285	Q15285	homo sapien
584	3	8.8	33	4	Q9P1T8	Q9plt8	homo sapien
585	3	8.8	33	4	Q9BV16	Q9bv16	homo sapien
586	3	8.8	33	4	Q92668	Q92668	homo sapien
587	3	8.8	33	5	Q9GTB2	Q9gtb2	eimeria ten
588	3	8.8	33	5	Q9GT93	Q9gt93	cryptospori
589	3	8.8	33	5	Q26673	Q26673	tethya aura
590	3	8.8	33	5	Q26672	Q26672	tethya aura
591	3	8.8	33	5	Q9GTC2	Q9gtc2	plasmodium
592	3	8.8	33	5	Q27637	Q27637	drosophila
593	3	8.8	33	5	Q9GTB3	Q9gtb3	eimeria ten
594	3	8.8	33	5	Q9GTA6	Q9gta6	sarcocystis
595	3	8.8	33	5	Q9GTA1	Q9gta1	babesia bov
596	3	8.8	33	5	Q17293	Q17293	cancer ante
597	3	8.8	33	5	Q27310	Q27310	paramecium
598	3	8.8	33	5	Q9GTA9	Q9gta9	sarcocystis
599	3	8.8	33	5	Q17147	Q17147	echinococcu
600	3	8.8	33	5	Q9GT95	Q9gt95	cryptospori
601	3	8.8	33	5	Q9GTA2	Q9gta2	babesia bov
602	3	8.8	33	5	Q9VHD7	Q9vhd7	drosophila
603	3	8.8	33	6	Q28788	Q28788	papio hamad
604	3	8.8	33	6	Q18916	Q18916	sus scrofa
605	3	8.8	33	6	Q9TSX7	Q9tsx7	sus scrofa
606	3	8.8	33	6	Q95M05	Q95m05	bos taurus
607	3	8.8	33	7	Q8MGU2	Q8mgu2	bos taurus
608	3	8.8	33	8	Q9BAC6	Q9bac6	euglena gra
609	3	8.8	33	8	Q8W9G0	Q8w9g0	meloidogyne
610	3	8.8	33	8	Q9BAC1	Q9bac1	euglena ste
611	3	8.8	33	8	Q78857	Q78857	phytophthor
612	3	8.8	33	8	Q9BAC4	Q9bac4	euglena mut
613	3	8.8	33	8	Q8WEJ5	Q8wej5	ginkgo bilo
614	3	8.8	33	8	Q8HUH3	Q8huh3	chlamydomon
615	3	8.8	33	8	Q8HS33	Q8hs33	hydrastis c
616	3	8.8	33	9	Q8SC41	Q8sc41	stx2 conver
617	3	8.8	33	9	Q38588	Q38588	bacterioph
618	3	8.8	33	9	Q38551	Q38551	bacterioph
619	3	8.8	33	9	Q8HA06	Q8ha06	bacterioph
620	3	8.8	33	10	Q49775	Q49775	arabidopsis
621	3	8.8	33	10	Q9S8V5	Q9s8v5	zea mays (m
622	3	8.8	33	10	Q9AYQ5	Q9ayq5	cucumis sat
623	3	8.8	33	11	Q9QVM2	Q9qvm2	mus sp. glu
624	3	8.8	33	11	Q62539	Q62539	mus spretus
625	3	8.8	33	12	Q72982	Q72982	hepatitis c
626	3	8.8	33	12	Q73068	Q73068	hepatitis c
627	3	8.8	33	12	Q90085	Q90085	human papil

628	3	8.8	33	12	072979	072979 hepatitis c
629	3	8.8	33	12	Q91J04	Q91j04 tt virus. o
630	3	8.8	33	12	072996	072996 hepatitis c
631	3	8.8	33	12	Q91J14	Q91j14 tt virus. o
632	3	8.8	33	12	072988	072988 hepatitis c
633	3	8.8	33	12	072992	072992 hepatitis c
634	3	8.8	33	12	Q91J12	Q91j12 tt virus. o
635	3	8.8	33	12	Q91J15	Q91j15 tt virus. o
636	3	8.8	33	12	Q91J07	Q91j07 tt virus. o
637	3	8.8	33	12	072995	072995 hepatitis c
638	3	8.8	33	12	Q91J09	Q91j09 tt virus. o
639	3	8.8	33	12	072990	072990 hepatitis c
640	3	8.8	33	12	073010	073010 hepatitis c
641	3	8.8	33	12	Q86912	Q86912 hepatitis c
642	3	8.8	33	12	Q8V5G7	Q8v5g7 hepatitis c
643	3	8.8	33	12	072981	072981 hepatitis c
644	3	8.8	33	12	Q91J08	Q91j08 tt virus. o
645	3	8.8	33	12	072997	072997 hepatitis c
646	3	8.8	33	12	073008	073008 hepatitis c
647	3	8.8	33	12	Q83963	Q83963 avian influ
648	3	8.8	33	12	072986	072986 hepatitis c
649	3	8.8	33	12	072993	072993 hepatitis c
650	3	8.8	33	12	Q91J06	Q91j06 tt virus. o
651	3	8.8	33	12	072984	072984 hepatitis c
652	3	8.8	33	12	073005	073005 hepatitis c
653	3	8.8	33	12	073067	073067 hepatitis c
654	3	8.8	33	12	072985	072985 hepatitis c
655	3	8.8	33	12	072999	072999 hepatitis c
656	3	8.8	33	12	Q91J16	Q91j16 tt virus. o
657	3	8.8	33	12	072998	072998 hepatitis c
658	3	8.8	33	12	Q91J11	Q91j11 tt virus. o
659	3	8.8	33	12	072994	072994 hepatitis c
660	3	8.8	33	12	Q8V5H0	Q8v5h0 hepatitis c
661	3	8.8	33	12	Q91J13	Q91j13 tt virus. o
662	3	8.8	33	12	Q8V5G8	Q8v5g8 hepatitis c
663	3	8.8	33	12	072983	072983 hepatitis c
664	3	8.8	33	12	073007	073007 hepatitis c
665	3	8.8	33	12	Q91J10	Q91j10 tt virus. o
666	3	8.8	33	12	072987	072987 hepatitis c
667	3	8.8	33	12	Q91J17	Q91j17 tt virus. o
668	3	8.8	33	12	Q69461	Q69461 human herpe
669	3	8.8	33	12	Q8V5G9	Q8v5g9 hepatitis c
670	3	8.8	33	12	072978	072978 hepatitis c
671	3	8.8	33	12	073009	073009 hepatitis c
672	3	8.8	33	12	073004	073004 hepatitis c
673	3	8.8	33	12	Q99138	Q99138 avian influ
674	3	8.8	33	13	P82740	P82740 rana tempor
675	3	8.8	33	13	P82236	P82236 rana tempor
676	3	8.8	33	15	Q9DZ98	Q9dz98 human immun
677	3	8.8	33	15	Q86107	Q86107 simian sarc
678	3	8.8	33	16	Q9PA23	Q9pa23 xylella fas
679	3	8.8	33	16	Q9KQP4	Q9kqp4 vibrio chol
680	3	8.8	33	16	Q9KML1	Q9kml1 vibrio chol
681	3	8.8	33	16	Q981J6	Q981j6 rhizobium l
682	3	8.8	33	16	Q97T91	Q97t91 streptococc
683	3	8.8	33	16	Q97PC1	Q97pc1 streptococc
684	3	8.8	33	16	Q932N2	Q932n2 staphylococ

685	3	8.8	33	16	Q8ZKL2	Q8zkl2	salmonella
686	3	8.8	33	16	Q8Z1V4	Q8z1v4	salmonella
687	3	8.8	33	16	Q8XAJ9	Q8xaj9	escherichia
688	3	8.8	33	16	Q8U5M4	Q8u5m4	agrobacteri
689	3	8.8	33	16	Q8VK01	Q8vk01	mycobacteri
690	3	8.8	33	16	Q8VIZ5	Q8viz5	mycobacteri
691	3	8.8	33	16	Q8NUL1	Q8nul1	staphylococ
692	3	8.8	33	16	Q8NT95	Q8nt95	corynebacte
693	3	8.8	33	16	Q8NLP2	Q8nlp2	corynebacte
694	3	8.8	33	16	Q8KG99	Q8kg99	chlorobium
695	3	8.8	33	16	Q8KBZ0	Q8kbz0	chlorobium
696	3	8.8	33	16	Q8G0U8	Q8g0u8	brucella su
697	3	8.8	33	16	Q8FZ67	Q8fz67	brucella su
698	3	8.8	33	16	Q8FY86	Q8fy86	brucella su
699	3	8.8	33	16	Q8FSG0	Q8fsg0	corynebacte
700	3	8.8	33	16	Q8EJH6	Q8ejh6	shewanella
701	3	8.8	33	16	Q8EGA9	Q8ega9	shewanella
702	3	8.8	33	16	Q8EE59	Q8ee59	shewanella
703	3	8.8	33	16	Q8EE42	Q8ee42	shewanella
704	3	8.8	33	16	Q8E8W4	Q8e8w4	shewanella
705	3	8.8	33	16	Q8E1Y5	Q8ely5	streptococc
706	3	8.8	33	16	Q8DWK4	Q8dwk4	streptococc
707	3	8.8	33	16	Q8CTR8	Q8ctr8	staphylococ
708	3	8.8	33	16	Q8CQY7	Q8cqy7	staphylococ
709	3	8.8	33	17	Q9HSX6	Q9hsx6	halobacteri
710	3	8.8	33	17	Q8U2X8	Q8u2x8	pyrococcus
711	3	8.8	34	2	Q54427	Q54427	spiroplasma
712	3	8.8	34	2	Q9X3L6	Q9x3l6	prochloroco
713	3	8.8	34	2	Q9R5U1	Q9r5u1	campylobact
714	3	8.8	34	2	Q43910	Q43910	azospirillu
715	3	8.8	34	2	Q44208	Q44208	pseudomonas
716	3	8.8	34	2	Q9X7J6	Q9x7j6	pseudomonas
717	3	8.8	34	2	Q8KYH2	Q8kyh2	bacillus an
718	3	8.8	34	2	O31061	O31061	butyrivibri
719	3	8.8	34	2	Q9R8A2	Q9r8a2	chlamydia t
720	3	8.8	34	2	Q9RZW6	Q9rzw6	borrelia bu
721	3	8.8	34	2	Q8GJC8	Q8gjc8	campylobact
722	3	8.8	34	2	Q8G8C9	Q8g8c9	pseudomonas
723	3	8.8	34	3	Q00377	Q00377	coccidioide
724	3	8.8	34	4	Q99910	Q99910	homo sapien
725	3	8.8	34	4	Q9H3R8	Q9h3r8	homo sapien
726	3	8.8	34	4	Q9UI64	Q9ui64	homo sapien
727	3	8.8	34	4	Q8WY57	Q8wy57	homo sapien
728	3	8.8	34	4	Q8WW51	Q8ww51	homo sapien
729	3	8.8	34	4	Q9BSP7	Q9bsp7	homo sapien
730	3	8.8	34	4	Q9BXC5	Q9bxc5	homo sapien
731	3	8.8	34	4	Q9H4L8	Q9h4l8	homo sapien
732	3	8.8	34	4	Q8NEQ3	Q8neq3	homo sapien
733	3	8.8	34	4	Q15251	Q15251	homo sapien
734	3	8.8	34	4	Q9NQY9	Q9nqy9	homo sapien
735	3	8.8	34	5	Q27821	Q27821	trichomonas
736	3	8.8	34	5	Q9GQE5	Q9gqe5	branchiosto
737	3	8.8	34	5	Q8N063	Q8n063	plasmodium
738	3	8.8	34	6	Q9TS91	Q9ts91	oryctolagus
739	3	8.8	34	6	Q8MJ92	Q8mj92	macaca mula
740	3	8.8	34	6	P79429	P79429	capra hircu
741	3	8.8	34	6	Q9TRI2	Q9tri2	sus scrofa

742	3	8.8	34	6	P82908	P82908 bos taurus
743	3	8.8	34	8	O79025	O79025 enallagma v
744	3	8.8	34	8	Q9T2T7	Q9t2t7 bos taurus
745	3	8.8	34	8	Q8MCA2	Q8mca2 phaseolus a
746	3	8.8	34	10	Q8W2H0	Q8w2h0 paspalum no
747	3	8.8	34	10	Q8VWL0	Q8vwl0 paspalum no
748	3	8.8	34	10	Q9SCA3	Q9sca3 lycopersico
749	3	8.8	34	10	P82137	P82137 spinacia ol
750	3	8.8	34	11	Q923Z1	Q923z1 mus musculu
751	3	8.8	34	11	Q8R557	Q8r557 mus musculu
752	3	8.8	34	11	Q9ET72	Q9et72 mus musculu
753	3	8.8	34	11	Q99KM9	Q99km9 mus musculu
754	3	8.8	34	11	Q99KX7	Q99kx7 mus musculu
755	3	8.8	34	11	Q64170	Q64170 mus sp. b-r
756	3	8.8	34	11	Q8VHL4	Q8vhl4 rattus norv
757	3	8.8	34	11	Q62534	Q62534 mus spretus
758	3	8.8	34	12	Q9DW68	Q9dw68 rat cytomeg
759	3	8.8	34	13	O42521	O42521 scyliorhinu
760	3	8.8	34	13	O13101	O13101 ambystoma m
761	3	8.8	34	13	Q8QGG2	Q8qgg2 oncorhynch
762	3	8.8	34	13	Q8QFM9	Q8qfm9 oncorhynch
763	3	8.8	34	13	O42526	O42526 scyliorhinu
764	3	8.8	34	13	Q9PRE7	Q9pre7 oryzias lat
765	3	8.8	34	13	Q8QGG1	Q8qgg1 oncorhynch
766	3	8.8	34	13	Q8QGF7	Q8qgf7 oncorhynch
767	3	8.8	34	13	Q98TM8	Q98tm8 platichthys
768	3	8.8	34	15	O40445	O40445 human immun
769	3	8.8	34	15	Q9WR32	Q9wr32 human immun
770	3	8.8	34	15	Q9Q593	Q9q593 human immun
771	3	8.8	34	15	Q9W8Y1	Q9w8y1 chimpanzee
772	3	8.8	34	16	O50812	O50812 borrelia bu
773	3	8.8	34	16	O50877	O50877 borrelia bu
774	3	8.8	34	16	Q9PGF8	Q9pgf8 xylella fas
775	3	8.8	34	16	Q9PFA5	Q9pfa5 xylella fas
776	3	8.8	34	16	Q9KRA8	Q9kra8 vibrio chol
777	3	8.8	34	16	Q9KPW9	Q9kpw9 vibrio chol
778	3	8.8	34	16	Q9KM63	Q9km63 vibrio chol
779	3	8.8	34	16	Q9K7C6	Q9k7c6 bacillus ha
780	3	8.8	34	16	Q9JY24	Q9jy24 neisseria m
781	3	8.8	34	16	Q9JVP3	Q9jvp3 neisseria m
782	3	8.8	34	16	Q9JUR9	Q9jur9 neisseria m
783	3	8.8	34	16	Q97SF7	Q97sf7 streptococc
784	3	8.8	34	16	Q97PI6	Q97pi6 streptococc
785	3	8.8	34	16	Q9K2B9	Q9k2b9 chlamydia p
786	3	8.8	34	16	Q8U5V2	Q8u5v2 agrobacteri
787	3	8.8	34	16	Q8VIY1	Q8viy1 mycobacteri
788	3	8.8	34	16	Q8RIC7	Q8ric7 fusobacteri
789	3	8.8	34	16	Q8NWX3	Q8nwx3 staphylococ
790	3	8.8	34	16	Q8NV10	Q8nv10 staphylococ
791	3	8.8	34	16	Q8KEQ8	Q8keq8 chlorobium
792	3	8.8	34	16	Q8KEL5	Q8kel5 chlorobium
793	3	8.8	34	16	Q8KDE4	Q8kde4 chlorobium
794	3	8.8	34	16	Q8G068	Q8g068 brucella su
795	3	8.8	34	16	Q8F897	Q8f897 leptospira
796	3	8.8	34	16	Q8F830	Q8f830 leptospira
797	3	8.8	34	16	Q8F827	Q8f827 leptospira
798	3	8.8	34	16	Q8F5Y7	Q8f5y7 leptospira

799	3	8.8	34	16	Q8F0V9	Q8f0v9 leptospira
800	3	8.8	34	16	Q8EZR6	Q8ezr6 leptospira
801	3	8.8	34	16	Q8EZ37	Q8ez37 leptospira
802	3	8.8	34	16	Q8EYW8	Q8eyw8 leptospira
803	3	8.8	34	16	Q8EYG6	Q8eyg6 leptospira
804	3	8.8	34	16	Q8EXH6	Q8exh6 leptospira
805	3	8.8	34	16	Q8EXA8	Q8exa8 leptospira
806	3	8.8	34	16	Q8EJ65	Q8ej65 shewanella
807	3	8.8	34	16	Q8EI45	Q8ei45 shewanella
808	3	8.8	34	16	Q8EHU5	Q8ehu5 shewanella
809	3	8.8	34	16	Q8E8Y3	Q8e8y3 shewanella
810	3	8.8	34	16	Q8E8W3	Q8e8w3 shewanella
811	3	8.8	34	16	Q8E173	Q8e173 streptococc
812	3	8.8	34	16	Q8CRY3	Q8cry3 staphylococ
813	3	8.8	34	17	Q8U1I1	Q8u1i1 pyrococcus
814	3	8.8	35	2	Q50052	Q50052 mycobacteri
815	3	8.8	35	2	Q9R624	Q9r624 bacillus su
816	3	8.8	35	2	Q9JPG9	Q9jpg9 neisseria m
817	3	8.8	35	2	Q9R625	Q9r625 bacillus su
818	3	8.8	35	2	Q9X3D6	Q9x3d6 prochloroco
819	3	8.8	35	2	Q9R5I3	Q9r5i3 thermoanaer
820	3	8.8	35	2	Q9FCX4	Q9fcx4 clostridium
821	3	8.8	35	2	Q9XBK0	Q9xbk0 bacillus ce
822	3	8.8	35	2	Q53564	Q53564 neisseria g
823	3	8.8	35	2	Q46537	Q46537 bacteroides
824	3	8.8	35	2	Q9ZG35	Q9zg35 chlamydia t
825	3	8.8	35	2	Q9RHG5	Q9rhg5 bacillus ce
826	3	8.8	35	2	Q9R4A1	Q9r4a1 klebsiella
827	3	8.8	35	2	O30661	O30661 vibrio chol
828	3	8.8	35	2	Q9ZG68	Q9zg68 chlamydia t
829	3	8.8	35	2	Q8RKG3	Q8rkg3 clostridium
830	3	8.8	35	2	Q8RIW2	Q8riw2 clostridium
831	3	8.8	35	2	Q9R626	Q9r626 bacillus su
832	3	8.8	35	2	P81927	P81927 lactobacill
833	3	8.8	35	3	Q96UT3	Q96ut3 saccharomyc
834	3	8.8	35	4	Q9BVR9	Q9bvr9 homo sapien
835	3	8.8	35	4	Q13380	Q13380 homo sapien
836	3	8.8	35	4	Q9BS62	Q9bs62 homo sapien
837	3	8.8	35	4	Q13165	Q13165 homo sapien
838	3	8.8	35	4	Q13828	Q13828 homo sapien
839	3	8.8	35	4	Q13264	Q13264 homo sapien
840	3	8.8	35	4	Q9Y634	Q9y634 homo sapien
841	3	8.8	35	4	Q9BU09	Q9bu09 homo sapien
842	3	8.8	35	4	Q8IU77	Q8iu77 homo sapien
843	3	8.8	35	5	Q27754	Q27754 pisaster oc
844	3	8.8	35	5	Q9U780	Q9u780 boophilus a
845	3	8.8	35	5	Q26372	Q26372 tribolium c
846	3	8.8	35	5	Q9U782	Q9u782 boophilus m
847	3	8.8	35	5	Q9TVJ7	Q9tvj7 boophilus m
848	3	8.8	35	5	Q9U783	Q9u783 boophilus m
849	3	8.8	35	5	Q9U784	Q9u784 boophilus m
850	3	8.8	35	5	Q9U781	Q9u781 boophilus m
851	3	8.8	35	5	Q8IF21	Q8if21 trypanosoma
852	3	8.8	35	6	Q95N74	Q95n74 equus cabal
853	3	8.8	35	6	Q9MZA7	Q9mza7 sus scrofa
854	3	8.8	35	8	Q951Q6	Q951q6 protoptilum
855	3	8.8	35	8	Q8W7S9	Q8w7s9 colpomenia

856	3	8.8	35	8	Q9GF85	Q9gf85 ginkgo bilo
857	3	8.8	35	8	Q8W7T0	Q8w7t0 petalonia b
858	3	8.8	35	8	Q8W7S8	Q8w7s8 petalonia f
859	3	8.8	35	8	Q8WE70	Q8we70 miliaria ca
860	3	8.8	35	8	Q8W7S7	Q8w7s7 scytosiphon
861	3	8.8	35	8	Q9GF98	Q9gf98 ceratophyll
862	3	8.8	35	8	Q95766	Q95766 cerataphis
863	3	8.8	35	8	Q94P82	Q94p82 corallium r
864	3	8.8	35	8	Q8WEJ7	Q8wej7 cycas circi
865	3	8.8	35	8	Q951S7	Q951s7 anothothela
866	3	8.8	35	8	Q951R1	Q951r1 narella nut
867	3	8.8	35	8	Q951S1	Q951s1 corallium k
868	3	8.8	35	8	Q8WII3	Q8wii3 colpomenia
869	3	8.8	35	8	Q951R3	Q951r3 anthomurice
870	3	8.8	35	8	Q8WIIH9	Q8wih9 scytosiphon
871	3	8.8	35	8	Q8WIIH5	Q8wih5 hydroclathr
872	3	8.8	35	8	Q951S9	Q951s9 protodendro
873	3	8.8	35	8	Q8WII1	Q8wii1 scytosiphon
874	3	8.8	35	8	Q951Q9	Q951q9 narella sp.
875	3	8.8	35	8	Q951S4	Q951s4 paragorgia
876	3	8.8	35	8	Q951R5	Q951r5 corallium s
877	3	8.8	35	10	Q9SPU2	Q9spu2 arabidopsis
878	3	8.8	35	10	Q9MAB1	Q9mab1 arabidopsis
879	3	8.8	35	10	P11785	P11785 triticum ae
880	3	8.8	35	10	Q9ZUW2	Q9zuw2 arabidopsis
881	3	8.8	35	10	Q9S9G9	Q9s9g9 lycopersico
882	3	8.8	35	10	P92971	P92971 arabidopsis
883	3	8.8	35	10	Q9LV08	Q9lv08 arabidopsis
884	3	8.8	35	10	Q942I4	Q942i4 oryza sativ
885	3	8.8	35	10	Q9LQ64	Q9lq64 arabidopsis
886	3	8.8	35	10	Q94IS4	Q94is4 pinus radia
887	3	8.8	35	10	Q39297	Q39297 brassica na
888	3	8.8	35	10	Q8RVJ7	Q8rvj7 populus eur
889	3	8.8	35	10	Q9FJ84	Q9fj84 arabidopsis
890	3	8.8	35	10	Q8GUX4	Q8gux4 picea maria
891	3	8.8	35	10	Q8GS04	Q8gs04 arabidopsis
892	3	8.8	35	11	Q9JM75	Q9jm75 mus musculu
893	3	8.8	35	11	Q63397	Q63397 rattus norv
894	3	8.8	35	11	Q9JLA4	Q9jla4 mus musculu
895	3	8.8	35	11	Q60608	Q60608 mus musculu
896	3	8.8	35	11	Q9QV50	Q9qv50 rattus sp.
897	3	8.8	35	11	Q9QV30	Q9qv30 rattus sp.
898	3	8.8	35	11	Q922H5	Q922h5 mus musculu
899	3	8.8	35	11	Q8BK89	Q8bk89 mus musculu
900	3	8.8	35	12	Q90151	Q90151 bombyx mori
901	3	8.8	35	12	Q65380	Q65380 banana bunc
902	3	8.8	35	12	Q83333	Q83333 murine hepa
903	3	8.8	35	12	O55549	O55549 measles vir
904	3	8.8	35	12	Q9YQW9	Q9yqw9 porcine cir
905	3	8.8	35	12	O91864	O91864 porcine cir
906	3	8.8	35	12	Q91HA8	Q91ha8 porcine cir
907	3	8.8	35	12	O93206	O93206 porcine cir
908	3	8.8	35	12	O56131	O56131 porcine cir
909	3	8.8	35	12	Q8BB50	Q8bb50 human papil
910	3	8.8	35	13	Q90XB5	Q90xb5 xenopus lae
911	3	8.8	35	13	P83224	P83224 oxyuranus m
912	3	8.8	35	13	P83225	P83225 oxyuranus s

913	3	8.8	35	13	P83227	P83227 oxyuranus m
914	3	8.8	35	13	P83228	P83228 oxyuranus s
915	3	8.8	35	13	P83229	P83229 oxyuranus s
916	3	8.8	35	13	P83226	P83226 oxyuranus s
917	3	8.8	35	15	Q75981	Q75981 human immun
918	3	8.8	35	15	Q70328	Q70328 human immun
919	3	8.8	35	15	Q70380	Q70380 human immun
920	3	8.8	35	15	Q70319	Q70319 human immun
921	3	8.8	35	15	Q79465	Q79465 human immun
922	3	8.8	35	15	Q70426	Q70426 human immun
923	3	8.8	35	15	Q9J3S2	Q9j3s2 human immun
924	3	8.8	35	15	O71950	O71950 human immun
925	3	8.8	35	15	Q9IPY2	Q9ipy2 human immun
926	3	8.8	35	15	Q80574	Q80574 human immun
927	3	8.8	35	15	Q9QR32	Q9qr32 human immun
928	3	8.8	35	15	Q9QR31	Q9qr31 human immun
929	3	8.8	35	15	Q9QR34	Q9qr34 human immun
930	3	8.8	35	15	Q70425	Q70425 human immun
931	3	8.8	35	15	Q9QR30	Q9qr30 human immun
932	3	8.8	35	15	Q70362	Q70362 human immun
933	3	8.8	35	15	Q80601	Q80601 human immun
934	3	8.8	35	15	Q8QDX6	Q8qdx6 human immun
935	3	8.8	35	15	Q77702	Q77702 human immun
936	3	8.8	35	15	Q9QR25	Q9qr25 human immun
937	3	8.8	35	15	Q9QFA0	Q9qfa0 human immun
938	3	8.8	35	15	Q70330	Q70330 human immun
939	3	8.8	35	15	Q77584	Q77584 human immun
940	3	8.8	35	15	Q76287	Q76287 human immun
941	3	8.8	35	15	Q70317	Q70317 human immun
942	3	8.8	35	15	Q70316	Q70316 human immun
943	3	8.8	35	15	Q9QQY6	Q9qqy6 human immun
944	3	8.8	35	15	Q70402	Q70402 human immun
945	3	8.8	35	15	Q9YM80	Q9ym80 human immun
946	3	8.8	35	15	Q8QDY0	Q8qdy0 human immun
947	3	8.8	35	15	Q75970	Q75970 human immun
948	3	8.8	35	15	Q8J3W4	Q8j3w4 human immun
949	3	8.8	35	15	Q70409	Q70409 human immun
950	3	8.8	35	15	Q70325	Q70325 human immun
951	3	8.8	35	15	Q9YM17	Q9ym17 human immun
952	3	8.8	35	15	Q79468	Q79468 human immun
953	3	8.8	35	15	Q9YM96	Q9ym96 human immun
954	3	8.8	35	15	Q70363	Q70363 human immun
955	3	8.8	35	15	Q70321	Q70321 human immun
956	3	8.8	35	15	Q9YM22	Q9ym22 human immun
957	3	8.8	35	15	Q75990	Q75990 human immun
958	3	8.8	35	15	Q70323	Q70323 human immun
959	3	8.8	35	15	Q75989	Q75989 human immun
960	3	8.8	35	15	Q70428	Q70428 human immun
961	3	8.8	35	15	Q9QR22	Q9qr22 human immun
962	3	8.8	35	15	Q9YM67	Q9ym67 human immun
963	3	8.8	35	15	Q77585	Q77585 human immun
964	3	8.8	35	15	Q70403	Q70403 human immun
965	3	8.8	35	15	Q9QR13	Q9qr13 human immun
966	3	8.8	35	15	Q70327	Q70327 human immun
967	3	8.8	35	15	Q77250	Q77250 human immun
968	3	8.8	35	15	Q75955	Q75955 human immun
969	3	8.8	35	15	Q9IPY4	Q9ipy4 human immun

970	3	8.8	35	15	O91412	O91412 human immun
971	3	8.8	35	15	Q70424	Q70424 human immun
972	3	8.8	35	15	Q77582	Q77582 human immun
973	3	8.8	35	16	O07593	O07593 bacillus su
974	3	8.8	35	16	Q9KR18	Q9kr18 vibrio chol
975	3	8.8	35	16	Q9KNU1	Q9knu1 vibrio chol
976	3	8.8	35	16	Q9JWX5	Q9jwx5 neisseria m
977	3	8.8	35	16	Q9K241	Q9k241 chlamydia p
978	3	8.8	35	16	Q8ZI89	Q8zi89 yersinia pe
979	3	8.8	35	16	Q8XZB7	Q8xzb7 ralstonia s
980	3	8.8	35	16	Q8X4F4	Q8x4f4 escherichia
981	3	8.8	35	16	Q8KCW5	Q8kcw5 chlorobium
982	3	8.8	35	16	Q8KCA6	Q8kca6 chlorobium
983	3	8.8	35	16	Q8G2D4	Q8g2d4 brucella su
984	3	8.8	35	16	Q8F9H5	Q8f9h5 leptospira
985	3	8.8	35	16	Q8F8D4	Q8f8d4 leptospira
986	3	8.8	35	16	Q8F1W8	Q8f1w8 leptospira
987	3	8.8	35	16	Q8EYH6	Q8eyh6 leptospira
988	3	8.8	35	16	Q8EGT2	Q8egt2 shewanella
989	3	8.8	35	16	Q8EGC0	Q8egc0 shewanella
990	3	8.8	35	16	Q8EEP3	Q8eep3 shewanella
991	3	8.8	35	16	Q8E9Z1	Q8e9z1 shewanella
992	3	8.8	35	16	Q8DUY1	Q8duy1 streptococc
993	3	8.8	35	17	Q9HMP1	Q9hmp1 halobacteri
994	3	8.8	35	17	Q8ZXX9	Q8zxx9 pyrobaculum
995	3	8.8	35	17	Q8ZWX8	Q8zwx8 pyrobaculum
996	3	8.8	36	2	O06954	O06954 salmonella
997	3	8.8	36	2	Q8VTS7	Q8vts7 listeria in
998	3	8.8	36	2	Q9ZG79	Q9zg79 chlamydia t
999	3	8.8	36	2	Q9RHE3	Q9rhe3 pediococcus
1000	3	8.8	36	2	Q8VTS5	Q8vts5 listeria we

ALIGNMENTS

RESULT 1

Q91Y90

ID Q91Y90 PRELIMINARY; PRT; 31 AA.
AC Q91Y90;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Peromyscus maniculatus (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF382953; AAK63072.1; -.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.

DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 41.2%; Score 14; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHL 15
|||||
Db 14 VSEIQLMHNLGKHL 27

RESULT 2

Q91Y91

ID Q91Y91 PRELIMINARY; PRT; 31 AA.
AC Q91Y91;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Peromyscus polionotus (Oldfield mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=42413;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF382952; AAK63071.1; -.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 41.2%; Score 14; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLGKHL 15
|||||
Db 14 VSEIQLMHNLGKHL 27

RESULT 3

O17148

ID O17148 PRELIMINARY; PRT; 34 AA.
AC O17148;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Antigen B/1 (Fragment).
 GN AGB/1.
 OS Echinococcus vogeli.
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidea; Taeniidae; Echinococcus.
 OX NCBI_TaxID=6213;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94359533; PubMed=8078520;
 RA Frosch P., Hartmann M., Muhlschlegel F., Frosch M.;
 RT "Sequence heterogeneity of the echinococcal antigen B.";
 RL Mol. Biochem. Parasitol. 64:171-175(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Haag K.L., Zaha A., Gottstein B.;
 RT "E. vogeli AgB/1 coding sequence.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF024665; AAB81611.1; -.
 FT NON_TER 1 1
 FT NON_TER 34 34
 SQ SEQUENCE 34 AA; 3964 MW; 3BE894E129CF84F3 CRC64;

Query Match 14.7%; Score 5; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28
 |||||
 Db 15 LRKKL 19

RESULT 4

Q97K50

ID Q97K50 PRELIMINARY; PRT; 34 AA.
 AC Q97K50;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Transcriptional regulator, AcrR family.
 GN CAC1071.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";

RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007622; AAK79045.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 4031 MW; 38D1A2A7C2F86E90 CRC64;

Query Match 14.7%; Score 5; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
|||||
Db 30 SVSEI 34

RESULT 5

Q9HR65

ID Q9HR65 PRELIMINARY; PRT; 34 AA.
AC Q9HR65;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Vng0840h.
GN VNG0840H.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005025; AAG19293.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 3731 MW; BA957904338DCD45 CRC64;

Query Match 14.7%; Score 5; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28
|||||
Db 26 LRKKL 30

RESULT 6

Q8BTB9

ID Q8BTB9 PRELIMINARY; PRT; 35 AA.
AC Q8BTB9;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Translin.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK011220; BAC25325.1; -.
 SQ SEQUENCE 35 AA; 3967 MW; F81156686390ECD8 CRC64;

Query Match 14.7%; Score 5; DB 11; Length 35;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
 |||||
 Db 2 SVSEI 6

RESULT 7

Q97RG6

ID Q97RG6 PRELIMINARY; PRT; 35 AA.
 AC Q97RG6;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein SP0853.
 GN SP0853.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae.";
 RL Science 293:498-506(2001).

DR EMBL; AE007391; AAK74982.1; -.
DR TIGR; SP0853; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 35 AA; 4276 MW; 6B8813CC028D6C7B CRC64;

Query Match 14.7%; Score 5; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQD 30
|||||
Db 30 KKLQD 34

RESULT 8

Q9BJE4

ID Q9BJE4 PRELIMINARY; PRT; 28 AA.
AC Q9BJE4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hox3-like protein (Fragment).
OS Pauropus sp. Wye-1996.
OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Pauropoda; Pauropodidae;
OC Pauropodinae; Pauropus.
OX NCBI_TaxID=146863;
RN [1]
RP SEQUENCE FROM N.A.
RA Cook C.E., Smith M.L., Telford M.J., Bastianello A., Akam M.E.;
RT "Hox genes and the phylogeny of the Arthropods."
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF335459; AAK28138.1; -.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3325 MW; 6A01E0EC23A843A5 CRC64;

Query Match 11.8%; Score 4; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 RRVE 22
|||||
Db 11 RRVE 14

RESULT 9

O24285

ID O24285 PRELIMINARY; PRT; 28 AA.
AC O24285;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LFY protein (Fragment).
GN LFY.
OS Pinus radiata (Monterey pine).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3347;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vegetative;
 RA Izquierdo L.Y., Vergara R.F., Alvarez-Buylla E.R.;
 RT "Partial characterization of Pinus radiata meristem identity homolog
 RT gene (LFY).";
 RL Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U66725; AAB06792.1; -.
 FT NON_TER 1 1
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3376 MW; 1736738622B4EE74 CRC64;

Query Match 11.8%; Score 4; DB 10; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
 ||||
 Db 15 LRKK 18

RESULT 10

Q8GZQ8

ID Q8GZQ8 PRELIMINARY; PRT; 28 AA.
 AC Q8GZQ8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE SNF-1 related kinase (Fragment).
 GN BKIN12.
 OS Hordeum vulgare var. distichum (Two-rowed barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=112509;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Igri;
 RA Clark J.S.C., Dani M., Barker J.H.A., Halford N.G., Karp A.;
 RT "Bkin12 Promoter Variants - Examples of Functional Biodiversity?";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF448389; AAN76447.1; -.
 KW Kinase.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 2950 MW; 853EDC11F6BB2C6C CRC64;

Query Match 11.8%; Score 4; DB 10; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
 ||||
 Db 18 NLGK 21

RESULT 11

Q49148

ID Q49148 PRELIMINARY; PRT; 29 AA.
 AC Q49148;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE PQQ biosynthesis polypeptide.
 GN PQQD.
 OS Methylobacterium extorquens.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Methylobacteriaceae; Methylobacterium.
 OX NCBI_TaxID=408;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AM1;
 RX MEDLINE=94179111; PubMed=8132470;
 RA Morris C.J., Biville F., Turlin E., Lee E., Ellermann K., Fan W.H.,
 RA Ramamoorthi R., Springer A.L., Lidstrom M.E.;
 RT "Isolation, phenotypic characterization, and complementation analysis
 RT of mutants of Methylobacterium extorquens AM1 unable to synthesize
 RT pyrroloquinoline quinone and sequences of pqqD, pqqG, and pqqC.";
 RL J. Bacteriol. 176:1746-1755(1994).
 DR EMBL; L25889; AAA17878.1; -.
 SQ SEQUENCE 29 AA; 3222 MW; B4831562CF76973C CRC64;

Query Match 11.8%; Score 4; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
 ||||
 Db 8 VSEI 11

RESULT 12

Q9UCL2

ID Q9UCL2 PRELIMINARY; PRT; 29 AA.
 AC Q9UCL2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Renal intestinal-type alkaline phosphatase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93092315; PubMed=1458595;
 RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
 RA Hirano K.;
 RT "Chemical nature of intestinal-type alkaline phosphatase in human
 RT kidney.";
 RL Clin. Chem. 38:2539-2542(1992).
 DR InterPro; IPR001952; Alk_phosphatase.

DR ProDom; PD001868; Alk_phosphatase; 1.
SQ SEQUENCE 29 AA; 3250 MW; 30501BB7BEEAD8D0 CRC64;

Query Match 11.8%; Score 4; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
||||
Db 23 KKLQ 26

RESULT 13

Q96PP3

ID Q96PP3 PRELIMINARY; PRT; 29 AA.
AC Q96PP3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lympho-epithelial Kazal type-related inhibitor LEKTI (Fragment).
GN SPINK5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sprecher E., Chavanas S., DiGiovanna J.J., Amin S., Nielsen K.,
RA Prendiville J.S., Silverman R., Esterly N.B., Spraker M.K., Guelig E.,
RA de Luna M.L., Williams M.L., Buehler B., Pfendner E., Bale S.J.,
RA Uitto J., Hovnanian A., Richard G.;
RT "The spectrum of pathogenic mutations in SPINK 5 in 19 families with
RT Netherton syndrome - Implications for mutation detection and first
RT case of prenatal diagnosis.";
RL J. Invest. Dermatol. 0:0-0(2001).
DR EMBL; AF295783; AAK97140.1; -.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3449 MW; 9F31E2AD857EC1BB CRC64;

Query Match 11.8%; Score 4; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
||||
Db 14 NLGK 17

RESULT 14

Q25603

ID Q25603 PRELIMINARY; PRT; 29 AA.
AC Q25603;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tubulin.

OS Onchocerca volvulus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Onchocerca.
 OX NCBI_TaxID=6282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chandrashekar R., Curtis K.C., Weil G.J.;
 RT "Onchocerca volvulus cDNA clone."
 RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U15095; AAA50364.1; -.
 SQ SEQUENCE 29 AA; 3539 MW; B917126A923EF884 CRC64;

Query Match 11.8%; Score 4; DB 5; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
 ||||
 Db 4 VSEI 7

RESULT 15

Q9TI61

ID Q9TI61 PRELIMINARY; PRT; 29 AA.
 AC Q9TI61;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Photosystem Q(B) protein (Fragment).
 GN PSBA.
 OS Allosyncarpia ternata.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Myrtaceae; Allosyncarpia.
 OX NCBI_TaxID=34307;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Udovicic F., Ladiges P.Y.;
 RT "Informativeness of nuclear and chloroplast DNA regions and the
 RT phylogeny of the eucalypts and related genera (Myrtaceae).";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF190370; AAF15265.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 SQ SEQUENCE 29 AA; 3501 MW; 977D8E6E67E1D833 CRC64;

Query Match 11.8%; Score 4; DB 8; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 VHNF 34
 ||||
 Db 7 VHNF 10

RESULT 16

O13043

ID O13043 PRELIMINARY; PRT; 29 AA.
AC O13043;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Whn transcription factor (Fragment).
GN WHN.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268658; PubMed=9108066;
RA Schlake T., Schorpp M., Nehls M., Boehm T.;
RT "The nude gene encodes a sequence-specific DNA binding protein with
RT homologs in organisms that lack an anticipatory immune system.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:3842-3847(1997).
DR EMBL; Y11539; CAA72302.1; -.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR ProDom; PD000425; TF_Fork_head; 1.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3243 MW; 62AE51F2BE7311E2 CRC64;

Query Match 11.8%; Score 4; DB 13; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
|||
Db 17 VSEI 20

RESULT 17

Q9REI5

ID Q9REI5 PRELIMINARY; PRT; 30 AA.
AC Q9REI5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Hypothetical 3.8 kDa protein.
OS Acidiphilium symbioticum.
OG Plasmid pAS3.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Acidiphilium.
OX NCBI_TaxID=94005;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KM2;
RA Mahapatra N.R., Ghosh S., Deb C., Banerjee P.C.;
RT "Cloning, sequencing and analysis of a cadmium and zinc resistance
RT conferring plasmid segment from Acidiphilium symbioticum KM2.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AJ239066; CAB65722.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 30 AA; 3766 MW; C1C02DAEEF51141C CRC64;

Query Match 11.8%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 MRRV 21
|||
Db 1 MRRV 4

RESULT 18

Q9JMV3

ID Q9JMV3 PRELIMINARY; PRT; 30 AA.
AC Q9JMV3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Luciferase alpha-subunit (Fragment).
GN LUXA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB101;
RA Lotz W., Bauer T.;
RT "luxAB/kan-cassette for site-directed insertion mutagenesis and
RT bacterial transcription studies.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HB101;
RA Olsson O., Koncz C., Szalay A.;
RT "The use of luxA gene of the bacterial luciferase operon as a reporter
RT gene.";
RL Mol. Gen. Genet. 215:1-9(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=HB101;
RX MEDLINE=92114868; PubMed=1685011;
RA Escher A., O'Kane D.J., Szalay A.;
RT "The beta subunit polypeptide of Vibrio harveyi luciferase determines
RT light emission at 42 degrees C.";
RL Mol. Gen. Genet. 230:385-393(1991).
DR EMBL; AJ249443; CAB96206.1; -.
DR HSSP; P07740; 1LUC.
DR InterPro; IPR002103; Bac_luciferase.
DR Pfam; PF00296; bac_luciferase; 1.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3454 MW; 2FC87235BDBE72FD CRC64;

Query Match 11.8%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
|||
Db 26 NLGK 29

RESULT 19

Q9UBV5

ID Q9UBV5 PRELIMINARY; PRT; 30 AA.

AC Q9UBV5;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Intestinal alkaline phosphatase (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=93092315; PubMed=1458595;

RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,

RA Hirano K.;

RT "Chemical nature of intestinal-type alkaline phosphatase in human

RT kidney.";

RL Clin. Chem. 38:2539-2542(1992).

DR InterPro; IPR001952; Alk_phosphatase.

DR ProDom; PD001868; Alk_phosphatase; 1.

SQ SEQUENCE 30 AA; 3349 MW; 30501BB7BEB9BDE6 CRC64;

Query Match 11.8%; Score 4; DB 4; Length 30;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 24 KKLQ 27

RESULT 20

Q8DZP7

ID Q8DZP7 PRELIMINARY; PRT; 30 AA.

AC Q8DZP7;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Hypothetical protein.

GN SAG1053.

OS Streptococcus agalactiae (serotype V).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=216466;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=2603 V/R / Serotype V;

RX MEDLINE=22222988; PubMed=12200547;

RA Tettelin H., Massignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
 RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
 RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
 RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative genomic analysis of an
 RT emerging human pathogen, serotype V *Streptococcus agalactiae*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
 DR EMBL; AE014240; AAM99934.1; -.
 DR TIGR; SAG1053; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 30 AA; 3492 MW; 8BC8F7525007AE91 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 23 KKLQ 26

RESULT 21

Q55314

ID Q55314 PRELIMINARY; PRT; 31 AA.
 AC Q55314;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Urf2 protein (Fragment).
 GN URF2.
 OS *Sulfolobus solfataricus*.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC *Sulfolobus*.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96085144; PubMed=8521845;
 RA Jones C.E., Fleming T.M., Cowan D.A., Littlechild J.A., Piper P.W.;
 RT "The phosphoglycerate kinase and glyceraldehyde-3-phosphate
 RT dehydrogenase genes from the thermophilic archaeon *Sulfolobus*
 RT *solfataricus* overlap by 8bp. Isolation, sequencing of the genes and
 RT expression on *Escherichia coli*.";
 RL Eur. J. Biochem. 233:800-808(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94082761; PubMed=8259927;
 RA Arcari P., Russo A.D., Ianniciello G., Gallo M., Bocchini V.;
 RT "Nucleotide sequence and molecular evolution of the gene coding for
 RT glyceraldehyde-3-phosphate dehydrogenase in the thermoacidophilic
 RT archaeobacterium *Sulfolobus solfataricus*.";
 RL Biochem. Genet. 31:241-251(1993).
 DR EMBL; X80178; CAA56461.1; -.

FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3554 MW; 9A2538F911C7309A CRC64;

Query Match 11.8%; Score 4; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
|||
Db 11 WLRK 14

RESULT 22

Q8NEI8

ID Q8NEI8 PRELIMINARY; PRT; 31 AA.
AC Q8NEI8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC030993; AAH30993.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 31 AA; 3437 MW; 72DCD0761839F7F7 CRC64;

Query Match 11.8%; Score 4; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
|||
Db 18 VSEI 21

RESULT 23

Q9MS77

ID Q9MS77 PRELIMINARY; PRT; 31 AA.
AC Q9MS77;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Photosystem I protein M.
GN PSAM.
OS Phacus acuminata.
OG Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Phacus.
OX NCBI_TaxID=130316;
RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21080550; PubMed=11212923;
 RA Doetsch N.A., Thompson M.D., Favreau M.R., Hallick R.B.;
 RT "Comparison of psbK operon organization and group III intron content
 RT in chloroplast genomes of 12 Euglenoid species.";
 RL Mol. Gen. Genet. 264:682-690(2001).
 DR EMBL; AF241276; AAF82438.1; -.
 KW Chloroplast.
 SQ SEQUENCE 31 AA; 3449 MW; 2FFB2AF4B4ACDEC8 CRC64;

Query Match 11.8%; Score 4; DB 8; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
 ||||
 Db 24 NLGK 27

RESULT 24

Q9PSU1

ID Q9PSU1 PRELIMINARY; PRT; 31 AA.
 AC Q9PSU1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Homeobox protein XlHbox8b (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipioidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA King M.W., Moore M.J.;
 RT "Expression of pattern regulating genes during bFGF-induced mesodermal
 RT differentiation in Xenopus.";
 RL Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U04865; AAA85027.1; -.
 DR HSSP; P14653; 1B72.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 FT NON_TER 1 1
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3921 MW; 75BF0F33C76937BD CRC64;

Query Match 11.8%; Score 4; DB 13; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 RRVE 22
 ||||
 Db 12 RRVE 15

RESULT 25

Q91816

ID Q91816 PRELIMINARY; PRT; 31 AA.
 AC Q91816;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Homeobox protein (Fragment).
 GN HOX-B2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA King M.W., Moore M.J.;
 RT "Expression of pattern regulating genes during bFGF-induced mesodermal
 RT differentiation in Xenopus."
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U04871; AAA85031.1; -.
 DR HSSP; P14653; 1B72.
 DR InterPro; IPR001356; Homeobox.
 DR Pfam; PF00046; homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR ProDom; PD000010; Homeobox; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 FT NON_TER 1 1
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3907 MW; F35A0791C519D508 CRC64;

Query Match 11.8%; Score 4; DB 13; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 RRVE 22
 ||||
 Db 12 RRVE 15

RESULT 26

O50669

ID O50669 PRELIMINARY; PRT; 31 AA.
 AC O50669;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein BBH11.
 GN BBH11.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OG Plasmid lp28-3.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;

RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, *Borrelia*
 RT burgdorferi.";
 RL Nature 390:580-586(1997).
 DR EMBL; AE000784; AAC66002.1; -.
 DR TIGR; BBH11; -.
 KW Hypothetical protein; Plasmid; Complete proteome.
 SQ SEQUENCE 31 AA; 3892 MW; 8C9F6B9E72D10FBA CRC64;

Query Match 11.8%; Score 4; DB 16; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 26 KKLQ 29

RESULT 27

Q00491

ID Q00491 PRELIMINARY; PRT; 32 AA.
 AC Q00491;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ORF protein (Fragment).
 OS *Streptomyces coelicolor*.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M145 ssp. A3(2);
 RX MEDLINE=91360338; PubMed=1715981;
 RA van Wezel G.P., Vijgenboom E., Bosch L.;
 RT "A comparative study of the ribosomal RNA operons of *Streptomyces*
 RT *coelicolor* A3(2) and sequence analysis of *rrnA*.";
 RL Nucleic Acids Res. 19:4399-4403(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M145 ssp. A3(2);
 RA van Wezel G.;
 RL Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; X60514; CAA43029.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 32 AA; 3617 MW; 3BCB81A239D8DD98 CRC64;

Query Match 11.8%; Score 4; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 RRVE 22
 ||||
Db 15 RRVE 18

RESULT 28

Q8KYN3

ID Q8KYN3 PRELIMINARY; PRT; 32 AA.
AC Q8KYN3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
GN BXA0100.
OS Bacillus anthracis.
OG Plasmid pX01.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2012;
RX MEDLINE=22061436; PubMed=12004073;
RA Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
RA Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
RA Keim P., Fraser C.M.;
RT "Comparative Genome Sequencing for Discovery of Novel Polymorphisms in
RT Bacillus anthracis."
RL Science 296:2028-2033(2002).
DR EMBL; AE011190; AAM26055.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 32 AA; 3921 MW; 393951048136BAFE CRC64;

Query Match 11.8%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 RRVE 22
 ||||
Db 19 RRVE 22

RESULT 29

Q9QZQ2

ID Q9QZQ2 PRELIMINARY; PRT; 32 AA.
AC Q9QZQ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neurotensin receptor (Fragment).
GN NTSR OR NTR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=99445567; PubMed=10514493;
 RA Tavares D., Tully K., Dobner P.R.;
 RT "Sequences required for induction of neurotensin receptor gene
 RT expression during neuronal differentiation of N1E-115 neuroblastoma
 RT cells.";
 RL J. Biol. Chem. 274:30066-30079(1999).
 DR EMBL; AF172326; AAD51806.1; -.
 DR MGD; MGI:97386; Ntsr.
 KW Receptor.
 FT NON_TER 32 32
 SQ SEQUENCE 32 AA; 3447 MW; 7F7EA4FA2CCF2EFB CRC64;

Query Match 11.8%; Score 4; DB 11; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HLNS 17
 ||||
 Db 2 HLNS 5

RESULT 30

Q9HSZ0

ID Q9HSZ0 PRELIMINARY; PRT; 32 AA.
 AC Q9HSZ0;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Vng0019h.
 GN VNG0019H.
 OS Halobacterium sp. (strain NRC-1).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
 RT "Genome sequence of Halobacterium species NRC-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AE004971; AAG18659.1; -.
 KW Complete proteome.
 SQ SEQUENCE 32 AA; 3758 MW; 22D669246C97A817 CRC64;

Query Match 11.8%; Score 4; DB 17; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
|||
Db 13 KLQD 16

RESULT 31

Q95SD4

ID Q95SD4 PRELIMINARY; PRT; 33 AA.
AC Q95SD4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GM02640p.
GN BCDNA:GM02640.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanenvong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY060847; AAL28395.1; -.
DR FlyBase; FBgn0047288; BcDNA:GM02640.
SQ SEQUENCE 33 AA; 3720 MW; 9C3FC1AEC9FBE4A7 CRC64;

Query Match 11.8%; Score 4; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 21 KKLQ 24

RESULT 32

Q9PKX3

ID Q9PKX3 PRELIMINARY; PRT; 33 AA.
AC Q9PKX3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein TC0337.
GN TC0337.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nigg;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RT pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 DR EMBL; AE002301; AAF39200.1; -.
 DR TIGR; TC0337; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 33 AA; 4075 MW; 1E7C5AD9BA5371EC CRC64;

Query Match 11.8%; Score 4; DB 16; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
 ||||
 Db 26 LRKK 29

RESULT 33

Q9ZG81

ID Q9ZG81 PRELIMINARY; PRT; 34 AA.
 AC Q9ZG81;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE ATP-dependent permease (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L2 434B;
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
 RT "Gene identification of Chlamydia trachomatis by random DNA
 RT sequencing.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF087260; AAD04038.1; -.
 FT NON_TER 1 1
 FT NON_TER 34 34
 SQ SEQUENCE 34 AA; 4186 MW; 3B38196393258A53 CRC64;

Query Match 11.8%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
 ||||
 Db 25 LRKK 28

RESULT 34

Q8GFK2

ID Q8GFK2 PRELIMINARY; PRT; 34 AA.
 AC Q8GFK2;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ORF37.
 OS Staphylococcus aureus.
 OG Plasmid EDINA plasmid.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-1;
 RA Sugai M., Yamaguchi T., Hayashi T., Nakasone K., Takami H.;
 RT "Complete nucleotide sequence of Staphylococcus aureus E-1 EDINA
 RT plasmid.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AP003089; BAC54529.1; -.
 KW Plasmid.
 SQ SEQUENCE 34 AA; 4138 MW; 88FBD773858BC6EE CRC64;

Query Match 11.8%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 6 KKLQ 9

RESULT 35

Q8C4P4

ID Q8C4P4 PRELIMINARY; PRT; 34 AA.
 AC Q8C4P4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Zinc finger homeodomain 4 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK081561; BAC38260.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 34 AA; 3755 MW; EF41DCAF348467B0 CRC64;

Query Match 11.8%; Score 4; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
||||
Db 2 KLQD 5

RESULT 36

Q90ZJ4

ID Q90ZJ4 PRELIMINARY; PRT; 34 AA.
AC Q90ZJ4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain long form (Fragment).
GN PDGF-A.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21363439; PubMed=11470524;
RA Horiuchi H., Inoue T., Furusawa S., Matsuda H.;
RT "Characterization and expression of three forms of cDNA encoding
RT chicken platelet-derived growth factor-A chain.";
RL Gene 272:181-190(2001).
DR EMBL; AB031024; BAB62544.1; -.
FT NON_TER 1 1
SQ SEQUENCE 34 AA; 3983 MW; FEF02F8A45B27DA5 CRC64;

Query Match 11.8%; Score 4; DB 13; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28
||||
Db 28 RKKL 31

RESULT 37

Q98FK5

ID Q98FK5 PRELIMINARY; PRT; 34 AA.
AC Q98FK5;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein msr3733.
GN MSR3733.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003002; BAB50562.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 34 AA; 3804 MW; D6AAA82ECB590413 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
 ||||
 Db 28 KLQD 31

RESULT 38

Q97FN0

ID Q97FN0 PRELIMINARY; PRT; 34 AA.
 AC Q97FN0;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Hypothetical protein CAC2698.
 GN CAC2698.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL; AE007767; AAK80645.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 34 AA; 4081 MW; E1CC1460EBADD9F6 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MRRV 21
 ||||
 Db 19 MRRV 22

RESULT 39

Q8G2Q2

ID Q8G2Q2 PRELIMINARY; PRT; 34 AA.
 AC Q8G2Q2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN BR0266.
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29461;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
 RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
 RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
 RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
 RT "The Brucella suis genome reveals fundamental similarities between
 RT animal and plant pathogens and symbionts."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 DR EMBL; AE014339; AAN29215.1; -.
 DR TIGR; BR0266; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 34 AA; 3781 MW; 76E820326E6CA66E CRC64;

Query Match 11.8%; Score 4; DB 16; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGKH 14
 ||||
 Db 10 LGKH 13

RESULT 40

Q15421

ID Q15421 PRELIMINARY; PRT; 35 AA.
 AC Q15421;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Simian sarcoma associated virus (SSAV)-related pol region DNA
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87071681; PubMed=2431542;
 RA Leib-Mosch C., Brack R., Werner T., Erfle V., Hehlmann R.;

RT "Isolation of an SSAV-related endogenous sequence from Human DNA.";
RL Virology 155:666-677(1986).
DR EMBL; M14911; AAA36592.1; -.
FT NON_TER 1 1
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 3742 MW; 2F70B02EE0BC86DF CRC64;

Query Match 11.8%; Score 4; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQDV 31
|||
Db 6 LQDV 9

Search completed: January 14, 2004, 10:41:54
Job time : 27.4206 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 5.61371 Seconds
(without alignments)
284.822 Million cell updates/sec

Title: US-09-843-221A-164
Perfect score: 34
Sequence: 1 SVSEIQLMHNLGKHLNSMRRVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1319

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	14.7	33	1	FABI_RHASA	P81175 rhamdia sap
2	4	11.8	29	1	DMD_RAT	P11530 rattus norv
3	4	11.8	30	1	ANF_RANRI	P09196 rana ridibu
4	4	11.8	35	1	ERFK_KLEAE	Q08599 klebsiella
5	4	11.8	39	1	PSBY_SYNY3	P73676 synechocyst
6	4	11.8	39	1	SR1C_SARPE	P08377 sarcophaga
7	3	8.8	28	1	CH60_MYCSM	P80673 mycobacteri
8	3	8.8	28	1	COXB_SOLTU	P80499 solanum tub
9	3	8.8	28	1	GUN_SCHCO	P81190 schizophyll
10	3	8.8	28	1	LPL_ECOLI	P09149 escherichia
11	3	8.8	28	1	PA23_TRIST	P82894 trimeresuru
12	3	8.8	28	1	PA2C_PSEPO	P20260 pseudechis
13	3	8.8	28	1	VI03_VACCP	Q00334 vaccinia vi
14	3	8.8	28	1	VIP_ALLMI	P48142 alligator m
15	3	8.8	28	1	VIP_RANRI	P81016 rana ridibu
16	3	8.8	28	1	VIP_SHEEP	P04565 ovis aries
17	3	8.8	29	1	GALA_ALLMI	P47215 alligator m

18	3	8.8	29	1	GALA_AMICA	P47214	amia calva
19	3	8.8	29	1	GALA_CHICK	P30802	gallus gall
20	3	8.8	29	1	GALA_ONCMY	P47213	oncorhynchu
21	3	8.8	29	1	GALA_RANRI	P47216	rana ridibu
22	3	8.8	29	1	GALA_SHEEP	P31234	ovis aries
23	3	8.8	29	1	GLUC_CHIBR	P31297	chinchilla
24	3	8.8	29	1	IPYR_DESVH	P19371	desulfovibr
25	3	8.8	29	1	NUO1_SOLTU	P80267	solanum tub
26	3	8.8	29	1	P2SM_LOXIN	P83046	loxosceles
27	3	8.8	29	1	PCG4_PACGO	P82417	pachycondyl
28	3	8.8	29	1	SODC_OLEEU	P80740	olea europa
29	3	8.8	29	1	TL16_SPIOL	P81834	spinacia ol
30	3	8.8	30	1	CBAL_BACST	P13722	bacillus st
31	3	8.8	30	1	DMS3_PHYSA	P80279	phyllomedus
32	3	8.8	30	1	FTN_BACFR	P28733	bacteroides
33	3	8.8	30	1	GLUM_ANGAN	P41521	anguilla an
34	3	8.8	30	1	OTCC_AERPU	P11726	aeromonas p
35	3	8.8	30	1	PCG2_PACGO	P82415	pachycondyl
36	3	8.8	30	1	PCG3_PACGO	P82416	pachycondyl
37	3	8.8	30	1	PRT1_CLUPA	P02335	clupea pall
38	3	8.8	30	1	PRTB_ONCMY	P12819	oncorhynchu
39	3	8.8	30	1	PSAM_PORPU	P51395	porphyra pu
40	3	8.8	30	1	RL18_HALCU	P05970	halobacteri
41	3	8.8	30	1	TX2_THRPR	P83476	thrixopelma
42	3	8.8	30	1	UP61_UPEIN	P82037	uperoleia i
43	3	8.8	30	1	UP62_UPEIN	P82038	uperoleia i
44	3	8.8	31	1	CEC1_PIG	P14661	sus scrofa
45	3	8.8	31	1	CXMA_CONMR	P56708	conus marmo
46	3	8.8	31	1	DEJP_DROME	P81160	drosophila
47	3	8.8	31	1	DIUX_DIPPU	P82372	diploptera
48	3	8.8	31	1	H13_WHEAT	P15872	triticum ae
49	3	8.8	31	1	LPL_BUCRP	Q53017	buchnera ap
50	3	8.8	31	1	MALK_PHOLU	P41124	photorhabdu
51	3	8.8	31	1	NAP4_HUMAN	P19877	homo sapien
52	3	8.8	31	1	PETL_LOTJA	Q9bbr4	lotus japon
53	3	8.8	31	1	PETL_MARPO	P12179	marchantia
54	3	8.8	31	1	PETL_MESVI	Q9mun4	mesostigma
55	3	8.8	31	1	PETL_NEPOL	Q9tky9	nephroselmi
56	3	8.8	31	1	PRT2_CLUPA	P02336	clupea pall
57	3	8.8	31	1	PSAM_EUGGR	P31479	euglena gra
58	3	8.8	31	1	SCK5_ANDMA	P31719	androctonus
59	3	8.8	31	1	SCKL_LEIQH	P16341	leiurus qui
60	3	8.8	31	1	Y822_BORBU	O51762	borrelia bu
61	3	8.8	32	1	ADHR_DROYA	P28487	drosophila
62	3	8.8	32	1	CAL2_ONCKE	P01264	oncorhynchu
63	3	8.8	32	1	CAL3_ONCKI	P01265	oncorhynchu
64	3	8.8	32	1	CAL_ANGJA	P01262	anguilla ja
65	3	8.8	32	1	CEC_OIKKI	P83420	oiketicus k
66	3	8.8	32	1	COA2_BPIF1	O80296	bacterioph
67	3	8.8	32	1	CY31_DESAC	P81078	desulfuromo
68	3	8.8	32	1	FF21_SALEN	P55224	salmonella
69	3	8.8	32	1	IAPP_PIG	Q29119	sus scrofa
70	3	8.8	32	1	LEC_DOLAX	P02875	dolichos ax
71	3	8.8	32	1	MIFH_TRITR	P81748	trichuris t
72	3	8.8	32	1	P1SM_LOXIN	P83045	loxosceles
73	3	8.8	32	1	PETM_GUITH	O78499	guillardia
74	3	8.8	32	1	PHSS_DESBN	P13064	desulfovibr

75	3	8.8	32	1	PRI3_ONCMY	P02330	oncorhynchu
76	3	8.8	32	1	PRT_ORYLA	Q91185	oryzias lat
77	3	8.8	32	1	PSAM_MARPO	P31590	marchantia
78	3	8.8	32	1	PSBQ_PEA	P19589	pisum sativ
79	3	8.8	32	1	PSBT_ODOSI	P49516	odontella s
80	3	8.8	32	1	PSBZ_EUGST	Q8sl89	euglena ste
81	3	8.8	32	1	PSBZ_EUGVI	Q8sl87	euglena vir
82	3	8.8	32	1	Y160_BPT4	P39247	bacterioph
83	3	8.8	32	1	YCPG_MASLA	P29735	mastigoclad
84	3	8.8	33	1	GGN1_RANRU	P80395	rana rugosa
85	3	8.8	33	1	GLU2_ORENI	P81027	oreochromis
86	3	8.8	33	1	MBP1_MAIZE	P28794	zea mays (m
87	3	8.8	33	1	PRI1_ONCMY	P02326	oncorhynchu
88	3	8.8	33	1	PRI2_ONCMY	P02328	oncorhynchu
89	3	8.8	33	1	PRTB_MUGCE	P08130	mugil cepha
90	3	8.8	33	1	RUGB_RANRU	P80955	rana rugosa
91	3	8.8	33	1	T1F_PARTE	Q27172	paramecium
92	3	8.8	33	1	Y50A_MYCTU	Q9cb56	mycobacteri
93	3	8.8	33	1	YC12_EUGGR	P31559	euglena gra
94	3	8.8	34	1	COXG_THUOB	P80976	thunnus obe
95	3	8.8	34	1	DMS1_PHYSA	P24302	phyllomedus
96	3	8.8	34	1	DMS2_PHYSA	P80278	phyllomedus
97	3	8.8	34	1	GAST_CAPHI	P04564	capra hircu
98	3	8.8	34	1	GUN1_SCLSC	P21833	sclerotinia
99	3	8.8	34	1	PRT1_SAROR	P25327	sarda orien
100	3	8.8	34	1	PRT1_SCOSC	P83264	scomber sco
101	3	8.8	34	1	PRT1_THUTH	P02321	thunnus thy
102	3	8.8	34	1	PRT2_SCOSC	P83265	scomber sco
103	3	8.8	34	1	PRT2_THUTH	P02322	thunnus thy
104	3	8.8	34	1	PRT_DICLA	Q9ps27	dicentrarch
105	3	8.8	34	1	TX1_SCOGR	P56855	scodra gris
106	3	8.8	35	1	CECA_AEDAL	P81417	aedes albop
107	3	8.8	35	1	COPA_CANFA	P40765	canis famil
108	3	8.8	35	1	CPI2_PIG	P80736	sus scrofa
109	3	8.8	35	1	GP58_BPSP1	O48412	bacterioph
110	3	8.8	35	1	HCYA_CHEDE	P83173	cherax dest
111	3	8.8	35	1	LEC1_CYTSE	P22970	cytissus ses
112	3	8.8	35	1	LEC3_ULEEU	P23032	ulex europe
113	3	8.8	35	1	NEF_HV1H3	P05854	human immun
114	3	8.8	35	1	NP30_STAAU	P21222	staphylococ
115	3	8.8	35	1	PBP_ORGPS	P34178	orgyia pseu
116	3	8.8	35	1	PETG_CYACA	Q9tlq9	cyanidium c
117	3	8.8	35	1	PSBM_SYNY3	P72701	synechocyst
118	3	8.8	35	1	RL15_SYNP7	P31160	synechococc
119	3	8.8	35	1	SCKK_TITSE	P56219	tityus serr
120	3	8.8	35	1	TX1_GRASP	P56852	grammostola
121	3	8.8	35	1	TX1_THRPR	P83480	thrixopelma
122	3	8.8	35	1	TX2_GRASP	P56853	grammostola
123	3	8.8	35	1	VORB_METTM	P80908	methanobact
124	3	8.8	35	1	Y210_HAEIN	P43964	haemophilus
125	3	8.8	35	1	YRKM_BACSU	P54440	bacillus su
126	3	8.8	36	1	ELH_THETS	P80594	theromyzon
127	3	8.8	36	1	NPF_ARTTR	P41334	artioposthi
128	3	8.8	36	1	OSTS_YEAST	Q99380	saccharomyc
129	3	8.8	36	1	PAHO_CHIBR	P41519	chinchilla
130	3	8.8	36	1	PETM_SYNY3	P74810	synechocyst
131	3	8.8	36	1	R18A_BOVIN	P82919	bos taurus

132	3	8.8	36	1	RET4_CHICK	P30370	gallus gall
133	3	8.8	36	1	RL6_HALCU	P05968	halobacteri
134	3	8.8	36	1	Y260_BACHD	Q9kg53	bacillus ha
135	3	8.8	37	1	DIU1_TENMO	P56618	tenebrio mo
136	3	8.8	37	1	IAPP_CRIGR	P19890	cricetulus
137	3	8.8	37	1	LCNM_LACLA	P83002	lactococcus
138	3	8.8	37	1	OGT1_RABIT	P81436	oryctolagus
139	3	8.8	37	1	PIP7_BOVIN	P21671	bos taurus
140	3	8.8	37	1	RK36_CHAGL	Q8m9v5	chaetosphae
141	3	8.8	37	1	RL36_MYCLE	Q9x7a2	mycobacteri
142	3	8.8	37	1	RL36_PASMU	P57942	pasteurella
143	3	8.8	37	1	SCKI_MESTA	P24663	mesobuthus
144	3	8.8	37	1	Y63_BPT3	P20328	bacterioph
145	3	8.8	37	1	YIM4_BPPH1	P10428	bacterioph
146	3	8.8	38	1	DNP_DENAN	P28374	dendroaspis
147	3	8.8	38	1	NLT1_VITSX	P80275	vitis sp. (
148	3	8.8	38	1	NLT2_VITSX	P33556	vitis sp. (
149	3	8.8	38	1	OBP2_HYSCR	P81648	hystrix cri
150	3	8.8	38	1	PSBY_CYAPA	P48272	cyanophora
151	3	8.8	38	1	PYSA_METBA	P80521	methanosarc
152	3	8.8	38	1	RL36_ECOLI	P21194	escherichia
153	3	8.8	38	1	RL36_PSEAE	Q9hwf6	pseudomonas
154	3	8.8	38	1	RL36_THEMA	Q9xli6	thermotoga
155	3	8.8	38	1	RL36_YERPE	Q8zj91	yersinia pe
156	3	8.8	38	1	RR12_PINCO	P49168	pinus conto
157	3	8.8	38	1	VG8_SPV4	P11340	spiroplasma
158	3	8.8	38	1	Y970_TREPA	O83936	treponema p
159	3	8.8	38	1	YJ39_ARCFU	O28340	archaeoglob
160	3	8.8	39	1	EXE3_HELHO	P20394	heloderma h
161	3	8.8	39	1	FUC3_RAT	P80349	rattus norv
162	3	8.8	39	1	GVPC_SPICC	P81000	spirulina s
163	3	8.8	39	1	H2A_BUFBG	P55897	bufo bufo g
164	3	8.8	39	1	LCGA_LACLA	P36961	lactococcus
165	3	8.8	39	1	PA2_AGKBI	Q9psf9	agkistrodon
166	3	8.8	39	1	PSBX_PORPU	P51197	porphyra pu
167	3	8.8	40	1	ALB1_TRASC	P81188	trachemys s
168	3	8.8	40	1	HPT_RABIT	P19007	oryctolagus
169	3	8.8	40	1	HS9A_RABIT	P30946	oryctolagus
170	3	8.8	40	1	KAD_STACA	P35141	staphylococ
171	3	8.8	40	1	PHRK_BACSU	O31840	bacillus su
172	3	8.8	40	1	PRE_BACLI	P18189	bacillus li
173	3	8.8	40	1	RK33_PEA	P51416	pisum sativ
174	3	8.8	40	1	RRPO_LSV	P27328	lily sympto
175	3	8.8	40	1	SAUV_PHYSA	P01144	phyllomedus
176	3	8.8	40	1	UC11_MAIZE	P80617	zea mays (m
177	3	8.8	40	1	VIT_MELGA	P56531	meleagris g
178	3	8.8	40	1	YDRB_STRPE	P32012	streptomyce
179	2	5.9	28	1	ACON_CANAL	P82611	candida alb
180	2	5.9	28	1	APC1_RABIT	P33047	oryctolagus
181	2	5.9	28	1	ARYA_PSEPU	P35902	pseudomonas
182	2	5.9	28	1	ARYC_NOCGL	P80008	nocardia gl
183	2	5.9	28	1	C1QC_RAT	P31722	rattus norv
184	2	5.9	28	1	ETX2_BACCE	P80568	bacillus ce
185	2	5.9	28	1	FIBA_CANFA	P02673	canis famil
186	2	5.9	28	1	FLA1_TREPH	P21988	treponema p
187	2	5.9	28	1	GDO_TRIMO	P02865	triticum mo
188	2	5.9	28	1	GRP_ALLMI	P31886	alligator m

189	2	5.9	28	1	GTS5_CHICK	P20137	gallus gall
190	2	5.9	28	1	GVPC_OSCAG	P80999	oscillator
191	2	5.9	28	1	HORC_HORSP	P02864	hordeum spo
192	2	5.9	28	1	HSP4_OCTVU	P83216	octopus vul
193	2	5.9	28	1	ICPP_VIPLE	P82475	vipera lebe
194	2	5.9	28	1	IORB_METTM	P80911	methanobact
195	2	5.9	28	1	ITR3_LUFCY	P35628	luffa cylin
196	2	5.9	28	1	LECA_IRIHO	P36230	iris hollan
197	2	5.9	28	1	LPFS_ECOLI	P22183	escherichia
198	2	5.9	28	1	LPL_SALTI	Q8z9h9	salmonella
199	2	5.9	28	1	LPL_SALTY	P03062	salmonella
200	2	5.9	28	1	LPW_SERMA	P03055	serratia ma
201	2	5.9	28	1	MAAI_RAT	P57113	rattus norv
202	2	5.9	28	1	MCDP_MEGPE	P04567	megabombus
203	2	5.9	28	1	NLT2_WHEAT	P39085	triticum ae
204	2	5.9	28	1	NXL1_BOUAN	P34074	boulengerin
205	2	5.9	28	1	OBP1_HYSCR	P81647	hystrix cri
206	2	5.9	28	1	OMPA_YERPS	P38399	yersinia ps
207	2	5.9	28	1	ORND_PLAOR	P25513	placobdella
208	2	5.9	28	1	OST1_CHICK	P80896	gallus gall
209	2	5.9	28	1	PA22_MICNI	P21791	micrurus ni
210	2	5.9	28	1	PA23_MICNI	P21792	micrurus ni
211	2	5.9	28	1	PETL_CYAPA	P48102	cyanophora
212	2	5.9	28	1	PHR_METTM	P58818	methanobact
213	2	5.9	28	1	PHYB_ASPFI	P81440	aspergillus
214	2	5.9	28	1	PP71_HCMVT	P24429	human cytom
215	2	5.9	28	1	PPOX_BOVIN	P56602	bos taurus
216	2	5.9	28	1	RL5_HALCU	P05972	halobacteri
217	2	5.9	28	1	RS19_PHYS1	O66093	phytoplasma
218	2	5.9	28	1	SCX2_BUTSI	P15230	buthus sind
219	2	5.9	28	1	SLP1_LEIQH	P80669	leiurus qui
220	2	5.9	28	1	SMS2_ORENI	P81029	oreochromis
221	2	5.9	28	1	TXO2_AGEAP	P15971	agelenopsis
222	2	5.9	28	1	VG9_SPV4	P11341	spiroplasma
223	2	5.9	28	1	VIP_DIDMA	P39089	didelphis m
224	2	5.9	28	1	VIP_SCYCA	P09685	scyliorhinu
225	2	5.9	28	1	Y073_ARCFU	O30163	archaeoglob
226	2	5.9	28	1	Y16P_BPT4	P39248	bacterioph
227	2	5.9	28	1	YA79_ARCFU	O29184	archaeoglob
228	2	5.9	29	1	12AH_CLOS4	P21215	clostridium
229	2	5.9	29	1	AL21_HORSE	P81216	equus cabal
230	2	5.9	29	1	AMEL_RABIT	P12761	oryctolagus
231	2	5.9	29	1	ATP9_PICPJ	Q06838	pichia pijp
232	2	5.9	29	1	ATPA_BRYMA	P26965	bryopsis ma
233	2	5.9	29	1	BR2D_RANES	P40840	rana escule
234	2	5.9	29	1	BREE_RANES	P40841	rana escule
235	2	5.9	29	1	CERB_CERCA	P36191	ceratitidis c
236	2	5.9	29	1	COA1_BPI22	P15413	bacterioph
237	2	5.9	29	1	COXJ_CANFA	Q9tr29	canis famil
238	2	5.9	29	1	COXK_SHEEP	Q9tr28	ovis aries
239	2	5.9	29	1	CU36_LOCFI	P11737	locusta mig
240	2	5.9	29	1	CXD6_CONGL	Q9twm7	conus glori
241	2	5.9	29	1	CXO7_CONGE	P05483	conus geogr
242	2	5.9	29	1	CXOC_CONMA	P37300	conus magus
243	2	5.9	29	1	CXOD_CONMA	Q26350	conus magus
244	2	5.9	29	1	CXST_CONGE	P58844	conus geogr
245	2	5.9	29	1	DMS5_PHYSA	P80281	phyllomedus

246	2	5.9	29	1	GLUC_ANAPL	P01276	anas platyr
247	2	5.9	29	1	GLUC_CALMI	P13189	callorhynch
248	2	5.9	29	1	GLUC_DIDMA	P18108	didelphis m
249	2	5.9	29	1	GLUC_LAMFL	Q9prq9	lampetra fl
250	2	5.9	29	1	GLUC_PLAFE	P23062	platichthys
251	2	5.9	29	1	GLUC_RABIT	P25449	oryctolagus
252	2	5.9	29	1	GLUC_TORMA	P09567	torpedo mar
253	2	5.9	29	1	H2B2_ECHES	P13282	echinus esc
254	2	5.9	29	1	HOXY_RHOOP	P22660	rhodococcus
255	2	5.9	29	1	HRJ_BOTJA	P20416	bothrops ja
256	2	5.9	29	1	HS98_NEUCR	P31540	neurospora
257	2	5.9	29	1	ITH3_BOVIN	P56652	bos taurus
258	2	5.9	29	1	ITR1_CUCMA	P01074	cucurbita m
259	2	5.9	29	1	ITR1_LUFCY	P25849	luffa cylin
260	2	5.9	29	1	ITR1_MOMRE	P17680	momordica r
261	2	5.9	29	1	ITR2_BRYDI	P11968	bryonia dio
262	2	5.9	29	1	ITR3_CYCPE	P83394	cyclanthera
263	2	5.9	29	1	ITR4_CYCPE	P83395	cyclanthera
264	2	5.9	29	1	ITR5_CYCPE	P83396	cyclanthera
265	2	5.9	29	1	KDPF_ECOLI	P36937	escherichia
266	2	5.9	29	1	MDH_BURPS	P80536	burkholderi
267	2	5.9	29	1	MULR_ECHML	P81798	echis multi
268	2	5.9	29	1	PETN_ANASP	Q913p6	anabaena sp
269	2	5.9	29	1	PETN_ARATH	P12178	arabidopsis
270	2	5.9	29	1	PETN_CHAGL	Q8ma13	chaetosphae
271	2	5.9	29	1	PETN_CYAPA	P48258	cyanophora
272	2	5.9	29	1	PETN_GUITH	O78498	guillardia
273	2	5.9	29	1	PETN_MAIZE	Q33302	zea mays (m
274	2	5.9	29	1	PETN_MARPO	P12177	marchantia
275	2	5.9	29	1	PETN_MESVI	Q9mus4	mesostigma
276	2	5.9	29	1	PETN_ODOSI	P49527	odontella s
277	2	5.9	29	1	PETN_PINTH	P41611	pinus thunb
278	2	5.9	29	1	PETN_PORPU	P51276	porphyra pu
279	2	5.9	29	1	PETN_PSINU	Q8wi23	psilotum nu
280	2	5.9	29	1	PETN_SKECO	O96807	skeletonema
281	2	5.9	29	1	PETN_SYNEL	Q8dkn2	synechococc
282	2	5.9	29	1	PETN_SYNY3	P72717	synechocyst
283	2	5.9	29	1	PK4_DICDI	P34103	dictyosteli
284	2	5.9	29	1	PRO1_DACGL	P18689	dactylis gl
285	2	5.9	29	1	PSAF_SYNP6	P31083	synechococc
286	2	5.9	29	1	PSAK_SPIOL	P14627	spinacia ol
287	2	5.9	29	1	PSAM_GUITH	O78448	guillardia
288	2	5.9	29	1	PSAX_SYNVU	P23320	synechococc
289	2	5.9	29	1	RL15_HALCU	P05971	halobacteri
290	2	5.9	29	1	RL15_STRLI	P49975	streptomyce
291	2	5.9	29	1	RP54_CLOKL	P38944	clostridium
292	2	5.9	29	1	RS7_METTE	O93639	methanosarc
293	2	5.9	29	1	SCX1_ANDMA	P56215	androctonus
294	2	5.9	29	1	SDHB_CLOPR	P80213	clostridium
295	2	5.9	29	1	SLP2_LEIQH	P80670	leiurus qui
296	2	5.9	29	1	SLP3_LEIQH	P80671	leiurus qui
297	2	5.9	29	1	TAT_HV1Z3	P12510	human immun
298	2	5.9	29	1	TLP_ACTDE	P81370	actinidia d
299	2	5.9	29	1	VARF_VIOAR	P58451	viola arven
300	2	5.9	29	1	Y15_BPT7	P03792	bacterioph
301	2	5.9	29	1	Y51_BPT3	P20326	bacterioph
302	2	5.9	29	1	YCX4_ODOSI	P49830	odontella s

303	2	5.9	29	1	YXCX_ODOSI	P49838	odontella s
304	2	5.9	30	1	2ENR_CLOTY	P11887	clostridium
305	2	5.9	30	1	A1AT_CHIVI	P38026	chinchilla
306	2	5.9	30	1	AATC_RABIT	P12343	oryctolagus
307	2	5.9	30	1	AATM_RABIT	P12345	oryctolagus
308	2	5.9	30	1	ACB1_DIGLA	P81624	digitalis l
309	2	5.9	30	1	AMPT_BACST	P00728	bacillus st
310	2	5.9	30	1	CALM_LYTPI	P05935	lytechinus
311	2	5.9	30	1	CH60_CLOPA	P81339	clostridium
312	2	5.9	30	1	CIRA_CHAPA	P56871	chassalia p
313	2	5.9	30	1	CLPA_PINPS	P81671	pinus pinas
314	2	5.9	30	1	COAE_CORAM	P58101	corynebacte
315	2	5.9	30	1	COXC_SOLTU	P80500	solanum tub
316	2	5.9	30	1	CRG2_SCOWA	P19865	scoliodon w
317	2	5.9	30	1	CX2A_CONBE	P58625	conus betul
318	2	5.9	30	1	CX7A_CONTU	P58923	conus tulip
319	2	5.9	30	1	CXEX_CONCN	P58928	conus conso
320	2	5.9	30	1	CXK4_CONST	P58921	conus stria
321	2	5.9	30	1	CXOB_CONPE	P56713	conus penna
322	2	5.9	30	1	CXVB_CONER	P58783	conus ermin
323	2	5.9	30	1	CY35_DESAC	P81079	desulfuromo
324	2	5.9	30	1	CY01_VIOOD	P82230	viola odora
325	2	5.9	30	1	CY08_VIOOD	P58440	viola odora
326	2	5.9	30	1	DEF2_MACMU	P82317	macaca mula
327	2	5.9	30	1	DIDH_COMTE	P80702	comamonas t
328	2	5.9	30	1	DIU2_HYLLI	P82015	hyles linea
329	2	5.9	30	1	DIU2_MANSE	P24858	manduca sex
330	2	5.9	30	1	FIBR_PANIN	P22775	panulirus i
331	2	5.9	30	1	HCY2_HOMAM	P82297	homarus ame
332	2	5.9	30	1	HETA_RADMA	P58691	radianthus
333	2	5.9	30	1	HSP5_OCTVU	P83217	octopus vul
334	2	5.9	30	1	HYPB_HYBPA	P58445	hybanthus p
335	2	5.9	30	1	IHFB_RHILE	P80606	rhizobium l
336	2	5.9	30	1	ITI1_LAGLE	P26771	lagenaria l
337	2	5.9	30	1	ITR1_CITLA	P11969	citrullus l
338	2	5.9	30	1	ITR1_MOMCH	P10294	momordica c
339	2	5.9	30	1	ITR2_ECBEL	P12071	ecballium e
340	2	5.9	30	1	ITR2_LUFCY	P25850	luffa cylin
341	2	5.9	30	1	ITR3_CUCMC	P32041	cucumis mel
342	2	5.9	30	1	ITR3_MOMCO	P82410	momordica c
343	2	5.9	30	1	ITR4_CUCSA	P10292	cucumis sat
344	2	5.9	30	1	ITR6_CYCPE	P83397	cyclanthera
345	2	5.9	30	1	ITR7_CYCPE	P83398	cyclanthera
346	2	5.9	30	1	KAB5_OLDAF	P58456	oldenlandia
347	2	5.9	30	1	LAS1_PIG	P80171	sus scrofa
348	2	5.9	30	1	LEAH_PHAVU	P81870	phaseolus v
349	2	5.9	30	1	MDH_HELGE	P80037	heliobacter
350	2	5.9	30	1	MMAL_DERMI	P16312	dermatophag
351	2	5.9	30	1	NU5M_PISOC	P24999	pisaster oc
352	2	5.9	30	1	NUO2_SOLTU	P80268	solanum tub
353	2	5.9	30	1	P2CO_ARTSP	P37365	arthrobacte
354	2	5.9	30	1	PCCA_MYXXA	P81185	myxococcus
355	2	5.9	30	1	PCG1_PACGO	P82414	pachycondyl
356	2	5.9	30	1	PCG5_PACGO	P82418	pachycondyl
357	2	5.9	30	1	PETN_NEPOL	Q9t101	nephroselmi
358	2	5.9	30	1	PLF4_RABIT	P83470	oryctolagus
359	2	5.9	30	1	PLMS_SQUAC	P82542	squalus aca

360	2	5.9	30	1	PMGY_CANAL	P82612	candida alb
361	2	5.9	30	1	PRT2_ONCMY	P02331	oncorhynchu
362	2	5.9	30	1	PRT3_ONCMY	P02332	oncorhynchu
363	2	5.9	30	1	PRT4_ONCMY	P02333	oncorhynchu
364	2	5.9	30	1	PSAM_CYACA	Q9tlx5	cyanidium c
365	2	5.9	30	1	PSAM_MESVI	Q9mus2	mesostigma
366	2	5.9	30	1	PSAM_ODOSI	P49487	odontella s
367	2	5.9	30	1	PSAM_PINTH	P41601	pinus thunb
368	2	5.9	30	1	PYSD_METBA	P80524	methanosarc
369	2	5.9	30	1	RIPS_MOMCO	P20655	momordica c
370	2	5.9	30	1	RKGG_LEPKE	P21587	lepidochely
371	2	5.9	30	1	SCK2_TITSE	P08816	tityus serr
372	2	5.9	30	1	SCX2_CENLI	P18927	centruroide
373	2	5.9	30	1	SILU_RHIPU	P02885	rhizomucor
374	2	5.9	30	1	TAT_HV1ZH	P12512	human immun
375	2	5.9	30	1	TL1X_SPIOL	P82537	spinacia ol
376	2	5.9	30	1	TL29_SPIOL	P81833	spinacia ol
377	2	5.9	30	1	TX2_HETVE	P58426	heteropoda
378	2	5.9	30	1	UC35_MAIZE	P80641	zea mays (m
379	2	5.9	30	1	UDDP_SULAC	P80143	sulfolobus
380	2	5.9	30	1	URE1_ECOLI	Q03284	escherichia
381	2	5.9	30	1	VAA1_EQUAR	Q04236	equisetum a
382	2	5.9	30	1	VAA1_PSINU	Q04237	psilotum nu
383	2	5.9	30	1	VAA2_EQUAR	Q04238	equisetum a
384	2	5.9	30	1	VAA2_PSINU	Q04239	psilotum nu
385	2	5.9	30	1	VATN_BOVIN	P81134	bos taurus
386	2	5.9	30	1	VG03_BPPF1	P25137	bacterioph
387	2	5.9	30	1	VPU_HV1SC	P05948	human immun
388	2	5.9	30	1	VTTA_BPT3	P20837	bacterioph
389	2	5.9	30	1	Y161_TREPA	O83196	treponema p
390	2	5.9	30	1	Y357_BORBU	O51332	borrelia bu
391	2	5.9	30	1	Y425_BORBU	O51386	borrelia bu
392	2	5.9	30	1	Y523_BORBU	O51473	borrelia bu
393	2	5.9	30	1	Y573_TREPA	O83583	treponema p
394	2	5.9	30	1	Y932_TREPA	O83902	treponema p
395	2	5.9	30	1	YCCB_ECOLI	P24244	escherichia
396	2	5.9	31	1	A98A_DROME	O46201	drosophila
397	2	5.9	31	1	BCAM_PIG	O19098	sus scrofa
398	2	5.9	31	1	CIRB_CHAPA	P56879	chassalia p
399	2	5.9	31	1	COG5_BOVIN	P83437	bos taurus
400	2	5.9	31	1	COX4_NEUCR	P06809	neurospora
401	2	5.9	31	1	CTRP_PENMO	P35002	penaeus mon
402	2	5.9	31	1	CU54_LOCFI	P11738	locusta mig
403	2	5.9	31	1	CXD6_CONNI	P56710	conus nigro
404	2	5.9	31	1	CXG6_CONTE	P58922	conus texti
405	2	5.9	31	1	CYLA_PSYLO	P56872	psychotria
406	2	5.9	31	1	DEF2_MESAU	P81466	mesocricetu
407	2	5.9	31	1	ENDB_CAMDR	P01203	camelus dro
408	2	5.9	31	1	ER29_BOVIN	P81623	bos taurus
409	2	5.9	31	1	ETFD_PARDE	P55932	paracoccus
410	2	5.9	31	1	FIBB_CANFA	P02677	canis famil
411	2	5.9	31	1	GP37_BPSP1	O48393	bacterioph
412	2	5.9	31	1	GT_SERMA	P22416	serratia ma
413	2	5.9	31	1	HBA_MACEU	P81043	macropus eu
414	2	5.9	31	1	HCY1_HOMAM	P82296	homarus ame
415	2	5.9	31	1	HCY2_MAISQ	P82303	maia squina
416	2	5.9	31	1	HEM2_PHAGO	P27687	phascolopsi

417	2	5.9	31	1	LC70_LACPA	P80959	lactobacill
418	2	5.9	31	1	LCCB_LEUME	P81052	leuconostoc
419	2	5.9	31	1	LPRM_ECOLI	P10739	escherichia
420	2	5.9	31	1	MDH_STRAR	P19982	streptomyce
421	2	5.9	31	1	PETL_ANASP	Q8yvg2	anabaena sp
422	2	5.9	31	1	PETL_ARATH	P56776	arabidopsis
423	2	5.9	31	1	PETL_BETVU	P46612	beta vulgar
424	2	5.9	31	1	PETL_CHLVU	P56306	chlorella v
425	2	5.9	31	1	PETL_GUITH	O78468	guillardia
426	2	5.9	31	1	PETL_MAIZE	P19445	zea mays (m
427	2	5.9	31	1	PETL_ODOSI	P49524	odontella s
428	2	5.9	31	1	PETL_OENHO	Q9mtk4	oenothera h
429	2	5.9	31	1	PETL_ORYSA	P12180	oryza sativ
430	2	5.9	31	1	PETL_PORPU	P51221	porphyra pu
431	2	5.9	31	1	PETL_PSINU	Q8wi03	psilotum nu
432	2	5.9	31	1	PETL_SPIOL	Q9m3l0	spinacia ol
433	2	5.9	31	1	PETL_WHEAT	P58247	triticum ae
434	2	5.9	31	1	PETM_CYACA	Q9t1r5	cyanidium c
435	2	5.9	31	1	PETN_CYACA	Q9t1r6	cyanidium c
436	2	5.9	31	1	PRT3_CLUPA	P02337	clupea pall
437	2	5.9	31	1	PSAK_ANAVA	P23317	anabaena va
438	2	5.9	31	1	PSAM_CHLVU	P56314	chlorella v
439	2	5.9	31	1	PSAM_CYAPA	P48185	cyanophora
440	2	5.9	31	1	PSBK_SYNVU	P19054	synechococc
441	2	5.9	31	1	PSBM_MESVI	Q9muq7	mesostigma
442	2	5.9	31	1	PSBT_CHLRE	P37256	chlamydomon
443	2	5.9	31	1	PSBT_CHLVU	P56327	chlorella v
444	2	5.9	31	1	PSBT_CYAPA	P48109	cyanophora
445	2	5.9	31	1	PSBT_EUGGR	P20176	euglena gra
446	2	5.9	31	1	PSBT_MESVI	Q9muv6	mesostigma
447	2	5.9	31	1	PSBT_PORPU	P51323	porphyra pu
448	2	5.9	31	1	PYSG_METBA	P80523	methanosarc
449	2	5.9	31	1	RECX_METCL	P37865	methylomona
450	2	5.9	31	1	RL21_STRTR	P48956	streptococc
451	2	5.9	31	1	SARL_HUMAN	O00631	homo sapien
452	2	5.9	31	1	SARL_MOUSE	Q9cqd6	mus musculu
453	2	5.9	31	1	SARL_RABIT	P42532	oryctolagus
454	2	5.9	31	1	SC37_MESMA	P83407	mesobuthus
455	2	5.9	31	1	SODC_STRHE	P81163	striga herm
456	2	5.9	31	1	TX3_HETVE	P58427	heteropoda
457	2	5.9	31	1	TXA3_PARAC	P09949	parasicyoni
458	2	5.9	31	1	Y191_BORBU	O51209	borrelia bu
459	2	5.9	31	1	Y3KD_BPCHP	P19187	bacterioph
460	2	5.9	31	1	Y603_ARCFU	O29652	archaeoglob
461	2	5.9	32	1	A2M_PACLE	P20738	pacifastacu
462	2	5.9	32	1	APL3_DIAGR	P81471	diatraea gr
463	2	5.9	32	1	ATP0_PIG	P80021	sus scrofa
464	2	5.9	32	1	ATP7_SPIOL	P80088	spinacia ol
465	2	5.9	32	1	ATPO_SPIOL	P80087	spinacia ol
466	2	5.9	32	1	B4G1_RAT	P80225	r beta-1,4-
467	2	5.9	32	1	CAAP_MICEC	P21162	micromonosp
468	2	5.9	32	1	CAL0_BOVIN	P01260	bos taurus
469	2	5.9	32	1	CAL0_PIG	P01259	sus scrofa
470	2	5.9	32	1	CAR1_ECHCA	Q9prp9	echis carin
471	2	5.9	32	1	COA1_BP1F1	O80295	bacterioph
472	2	5.9	32	1	COA1_BPIKE	P03676	bacterioph
473	2	5.9	32	1	COA2_BPFD	P03677	bacterioph

474	2	5.9	32	1	CRP_PLEPL	P12245	pleuronecte
475	2	5.9	32	1	CXG7_CONPE	P56711	conus penna
476	2	5.9	32	1	CYBL_RHOGR	P32953	rhodotorula
477	2	5.9	32	1	CYSB_FASHE	P80529	fasciola he
478	2	5.9	32	1	DBH_SYNY1	P02343	synechocyst
479	2	5.9	32	1	ER29_CHICK	P81628	gallus gall
480	2	5.9	32	1	ER29_TRIVU	P81629	trichosurus
481	2	5.9	32	1	ERH_PIG	P80230	sus scrofa
482	2	5.9	32	1	FER_PORCR	P18821	porphyridiu
483	2	5.9	32	1	FLA1_METHU	P17603	methanospir
484	2	5.9	32	1	FRIH_ANAPL	P80145	anas platyr
485	2	5.9	32	1	GHR4_RAT	P33581	rattus norv
486	2	5.9	32	1	GLB4_LAMSP	P20413	lamellibrac
487	2	5.9	32	1	GT82_DICLA	P82608	dicentrarch
488	2	5.9	32	1	H2AZ_ONCMY	P22647	oncorhynchu
489	2	5.9	32	1	HCCY_CHEDE	P83172	cherax dest
490	2	5.9	32	1	IAPP_BOVIN	Q28207	bos taurus
491	2	5.9	32	1	IAPP_SAGOE	Q28934	saguinus oe
492	2	5.9	32	1	IAPP_SHEEP	Q28605	ovis aries
493	2	5.9	32	1	ILVB_ENTAE	Q09129	enterobacte
494	2	5.9	32	1	ITR2_CUCSA	P10291	cucumis sat
495	2	5.9	32	1	ITR3_CUCPE	P10293	cucurbita p
496	2	5.9	32	1	ITR4_CUCMA	P07853	cucurbita m
497	2	5.9	32	1	LPID_ECOLI	P03060	escherichia
498	2	5.9	32	1	LPID_EDWTA	P08140	edwardsiell
499	2	5.9	32	1	LPIV_ECOLI	P03061	escherichia
500	2	5.9	32	1	MDH_NITAL	P10887	nitzschia a
501	2	5.9	32	1	NEUB_PIG	P01297	sus scrofa
502	2	5.9	32	1	OVOS_ANAPL	P20739	anas platyr
503	2	5.9	32	1	PA22_AGKHP	P18997	agkistrodon
504	2	5.9	32	1	PA2_RHONO	P43318	rhopilema n
505	2	5.9	32	1	PETL_CHLRE	P50369	chlamydomon
506	2	5.9	32	1	PETM_PORPU	P51275	porphyra pu
507	2	5.9	32	1	PHNS_DESMU	P13062	desulfovibr
508	2	5.9	32	1	PRT1_ESOLU	P02325	esox lucius
509	2	5.9	32	1	PRT1_ONCKE	P02327	oncorhynchu
510	2	5.9	32	1	PRT4_SCYCA	P30259	scyliorhinu
511	2	5.9	32	1	PRT5_ONCMY	P02334	oncorhynchu
512	2	5.9	32	1	PRT6_ONCMY	P08145	oncorhynchu
513	2	5.9	32	1	PRT7_ONCMY	P08146	oncorhynchu
514	2	5.9	32	1	PRT8_ONCMY	P12817	oncorhynchu
515	2	5.9	32	1	PRT9_ONCMY	P08147	oncorhynchu
516	2	5.9	32	1	PRTA_ONCMY	P12818	oncorhynchu
517	2	5.9	32	1	PRTE_HALME	P28308	halobacteri
518	2	5.9	32	1	PSBT_CYACA	O19927	cyanidium c
519	2	5.9	32	1	PSBT_GUITH	O78512	guillardia
520	2	5.9	32	1	PSBZ_EUGAN	Q8s195	euglena ana
521	2	5.9	32	1	PSBZ_EUGGA	Q8s193	euglena gra
522	2	5.9	32	1	PSBZ_EUGMY	Q8s191	euglena myx
523	2	5.9	32	1	RIP2_PHYDI	P34967	phytolacca
524	2	5.9	32	1	RK1_RABIT	P81655	oryctolagus
525	2	5.9	32	1	RS19_YEREN	Q56847	yersinia en
526	2	5.9	32	1	SCK2_CENNO	P58504	centruroides
527	2	5.9	32	1	TAT_SIVM2	P05912	simian immu
528	2	5.9	32	1	TRYP_PENMO	P35050	penaeus mon
529	2	5.9	32	1	TX29_PHONI	P29426	phoneutria
530	2	5.9	32	1	TXP7_APTSC	P49271	aptostichus

531	2	5.9	32	1	UC09_MAIZE	P80615	zea mays (m
532	2	5.9	32	1	Y169_TREPA	O83199	treponema p
533	2	5.9	32	1	Y433_BORBU	O51394	borrelia bu
534	2	5.9	32	1	YH17_HAEIN	P44295	haemophilus
535	2	5.9	32	1	YSCA_YEREN	Q01242	yersinia en
536	2	5.9	32	1	YTK3_ILTVT	P23985	infectious
537	2	5.9	33	1	ACT_DICVI	Q24733	dictyocaulu
538	2	5.9	33	1	ALOX_PICPA	P04842	pichia past
539	2	5.9	33	1	ANP3_MYOSC	P04367	myoxocephal
540	2	5.9	33	1	ANP5_MYOAE	P20421	myoxocephal
541	2	5.9	33	1	ATP7_SOLTU	P80496	solanum tub
542	2	5.9	33	1	BR2A_RANES	P40837	rana escule
543	2	5.9	33	1	BR2B_RANES	P40838	rana escule
544	2	5.9	33	1	BR2E_RANES	P32413	rana escule
545	2	5.9	33	1	BR2_RANBP	P32424	rana brevip
546	2	5.9	33	1	CECB_HELVI	P83414	heliiothis v
547	2	5.9	33	1	CECC_HELVI	P83415	heliiothis v
548	2	5.9	33	1	COA1_BPFD	P03675	bacterioph
549	2	5.9	33	1	COA2_BPIKE	P03678	bacterioph
550	2	5.9	33	1	COXL_ONCMY	P80330	oncorhynch
551	2	5.9	33	1	CU89_HUMAN	P59042	homo sapien
552	2	5.9	33	1	CXBW_CONRA	P58804	conus radia
553	2	5.9	33	1	CXO_CONVE	P83301	conus ventr
554	2	5.9	33	1	DBB2_DOLAU	P83376	dolabella a
555	2	5.9	33	1	DEF1_MESAU	P81465	mesocricetu
556	2	5.9	33	1	DEF3_MESAU	P81467	mesocricetu
557	2	5.9	33	1	DEF4_MESAU	P81468	mesocricetu
558	2	5.9	33	1	DHE3_PIG	P42174	sus scrofa
559	2	5.9	33	1	FER_PORAE	P18820	porphyridiu
560	2	5.9	33	1	GAST_CAVPO	P06885	cavia porce
561	2	5.9	33	1	GAST_CHIBR	P10034	chinchilla
562	2	5.9	33	1	GAST_DIDMA	P33713	didelphis m
563	2	5.9	33	1	GGN2_RANRU	P80396	rana rugosa
564	2	5.9	33	1	GGN3_RANRU	P80397	rana rugosa
565	2	5.9	33	1	HF40_MAIZE	P82865	zea mays (m
566	2	5.9	33	1	HOXU_RHOOP	P22659	rhodococcus
567	2	5.9	33	1	LPPY_SALTY	P08522	salmonella
568	2	5.9	33	1	LPRH_ECOLI	P37324	escherichia
569	2	5.9	33	1	LYC2_HORSE	P81710	equus cabal
570	2	5.9	33	1	MHAA_STRCH	P80435	streptomyce
571	2	5.9	33	1	MYMY_MYTED	P81614	mytilus edu
572	2	5.9	33	1	OTCC_PSEPU	P11727	pseudomonas
573	2	5.9	33	1	PEN3_ADECU	P35987	canine aden
574	2	5.9	33	1	PETM_CYAPA	P48366	cyanophora
575	2	5.9	33	1	PETM_SYNEL	Q8dj15	synechococc
576	2	5.9	33	1	PK1_DICDI	P34101	dictyosteli
577	2	5.9	33	1	PK5_DICDI	P34104	dictyosteli
578	2	5.9	33	1	PRTL_ECOLI	P02338	escherichia
579	2	5.9	33	1	PSAI_SPIOL	P17228	spinacia ol
580	2	5.9	33	1	PSAK_CUCSA	P42051	cucumis sat
581	2	5.9	33	1	PSBT_ARATH	P37259	arabidopsis
582	2	5.9	33	1	PSBT_MAIZE	P37257	zea mays (m
583	2	5.9	33	1	RL21_XENLA	P49628	xenopus lae
584	2	5.9	33	1	RL26_XENLA	P49629	xenopus lae
585	2	5.9	33	1	RL28_XENLA	P46780	xenopus lae
586	2	5.9	33	1	RL4_HALCU	P05967	halobacteri
587	2	5.9	33	1	RPOC_HETCA	P36441	heterosigma

588	2	5.9	33	1	RRPO_BP BZ1	P09674	bacterioph
589	2	5.9	33	1	RS4_XENLA	P49401	xenopus lae
590	2	5.9	33	1	RT25_BOVIN	P82669	bos taurus
591	2	5.9	33	1	RUGA_RANRU	P80954	rana rugosa
592	2	5.9	33	1	SCX9_BUTOC	P04099	buthus occi
593	2	5.9	33	1	THIO_CLOST	P81109	clostridium
594	2	5.9	33	1	TX1_HETVE	P58425	heteropoda
595	2	5.9	33	1	TXH1_SELHU	P56676	selenocosmi
596	2	5.9	33	1	TXN3_SELHA	P83464	selenocosmi
597	2	5.9	33	1	VT1B_RAT	P58200	rattus norv
598	2	5.9	33	1	Y474_BORBU	O51430	borrelia bu
599	2	5.9	33	1	Y656_TREPA	O83662	treponema p
600	2	5.9	33	1	Y849_BORBU	O51789	borrelia bu
601	2	5.9	33	1	YC12_CHLRE	P50370	chlamydomon
602	2	5.9	33	1	YC12_MARPO	P31560	marchantia
603	2	5.9	33	1	YC12_MESVI	Q9mus3	mesostigma
604	2	5.9	33	1	YC12_NEPOL	Q9tky6	nephroselmi
605	2	5.9	33	1	YC12_PINTH	P41600	pinus thunb
606	2	5.9	33	1	YL74_ARCFU	O28108	archaeoglob
607	2	5.9	33	1	YLCH_BP82	Q37869	bacterioph
608	2	5.9	33	1	YLCH_ECOLI	Q47268	escherichia
609	2	5.9	34	1	AMP2_CHICK	P80390	gallus gall
610	2	5.9	34	1	ASPG_PIG	P30918	sus scrofa
611	2	5.9	34	1	BR2C_RANES	P40839	rana escule
612	2	5.9	34	1	BUTH_ANDAU	P56685	androctonus
613	2	5.9	34	1	COL_CHICK	P11148	gallus gall
614	2	5.9	34	1	COXA_THETH	P82543	thermus the
615	2	5.9	34	1	CXGS_CONGE	P15472	conus geogr
616	2	5.9	34	1	DEF2_RABIT	P07468	oryctolagus
617	2	5.9	34	1	DEF7_RABIT	P80223	oryctolagus
618	2	5.9	34	1	ECAB_ECTTU	P49344	ectatomma t
619	2	5.9	34	1	EF2_RABIT	P55823	oryctolagus
620	2	5.9	34	1	EGGR_APLCA	P01363	aplysia cal
621	2	5.9	34	1	H1S_STRPU	P19376	strongyloce
622	2	5.9	34	1	HS7S_CUCMA	P31082	cucurbita m
623	2	5.9	34	1	ITR1_MOMCO	P82408	momordica c
624	2	5.9	34	1	ITR2_MOMCO	P82409	momordica c
625	2	5.9	34	1	LPTN_PROVU	P28779	proteus vul
626	2	5.9	34	1	M44E_HUMAN	Q96pg1	homo sapien
627	2	5.9	34	1	MYTA_MYTED	P81612	mytilus edu
628	2	5.9	34	1	MYTB_MYTED	P81613	mytilus edu
629	2	5.9	34	1	PETM_ANASP	Q9f4w2	anabaena sp
630	2	5.9	34	1	PRT_PERFV	P29629	perca flave
631	2	5.9	34	1	PSAI_LOTJA	Q9bbs0	lotus japon
632	2	5.9	34	1	PSAI_OENHO	Q9mtl2	oenothera h
633	2	5.9	34	1	PSAI_SOYBN	P49159	glycine max
634	2	5.9	34	1	PSBM_ARATH	P12169	arabidopsis
635	2	5.9	34	1	PSBM_CHLRE	P92277	chlamydomon
636	2	5.9	34	1	PSBM_MARPO	P12168	marchantia
637	2	5.9	34	1	PSBM_NEPOL	Q9tl37	nephroselmi
638	2	5.9	34	1	PSBM_OENHO	Q9mtm8	oenothera h
639	2	5.9	34	1	PSBM_PEA	P34833	pisum sativ
640	2	5.9	34	1	PSBM_WHEAT	Q9xps6	triticum ae
641	2	5.9	34	1	PSBT_TOBAC	P12184	nicotiana t
642	2	5.9	34	1	PSPC_BOVIN	P15783	bos taurus
643	2	5.9	34	1	PSPC_CANFA	P22397	canis famil
644	2	5.9	34	1	PYSB_METBA	P80522	methanosarc

645	2	5.9	34	1	RNL1_PIG	P15466	sus scrofa
646	2	5.9	34	1	RR2_OCHNE	Q40606	ochrosphaer
647	2	5.9	34	1	SCXM_SCOMA	P80719	scorpio mau
648	2	5.9	34	1	SMS_MYXGL	P19209	myxine glut
649	2	5.9	34	1	THEM_MALSU	P13858	malbranchea
650	2	5.9	34	1	TX33_PHONI	P81789	phoneutria
651	2	5.9	34	1	TXP5_BRASM	P49266	brachypelma
652	2	5.9	34	1	VLYS_BPM1	P08229	bacterioph
653	2	5.9	34	1	VPU_HV1W2	P08808	human immun
654	2	5.9	34	1	Y05J_BPT4	P39239	bacterioph
655	2	5.9	34	1	Y224_TREPA	O83253	treponema p
656	2	5.9	34	1	Y848_BORBU	O51788	borrelia bu
657	2	5.9	34	1	Y870_HAEIN	P44065	haemophilus
658	2	5.9	34	1	Y967_HAEIN	P44086	haemophilus
659	2	5.9	34	1	YC12_GUITH	O78460	guillardia
660	2	5.9	34	1	YC12_ODOSI	P49529	odontella s
661	2	5.9	34	1	YC12_PORPU	P51385	porphyra pu
662	2	5.9	34	1	YC12_SKECO	O96797	skeletonema
663	2	5.9	34	1	YMIA_AGRTU	P38437	agrobacteri
664	2	5.9	34	1	Z33B_HUMAN	Q06731	homo sapien
665	2	5.9	35	1	ADO1_AGRDO	P58608	agriosphodr
666	2	5.9	35	1	C550_BACHA	P80091	bacillus ha
667	2	5.9	35	1	CEC4_BOMMO	P14666	bombyx mori
668	2	5.9	35	1	CECA_HELVI	P83413	heliopsis v
669	2	5.9	35	1	CECB_ANTPE	P01509	antheraea p
670	2	5.9	35	1	CHI1_CASSA	P29137	castanea sa
671	2	5.9	35	1	D3HI_RABIT	P32185	oryctolagus
672	2	5.9	35	1	DEFB_MYTED	P81611	mytilus edu
673	2	5.9	35	1	END4_YEREN	P42691	yersinia en
674	2	5.9	35	1	EXE2_HELVS	P04204	heloderma s
675	2	5.9	35	1	FAS_CAPHI	P08757	capra hircu
676	2	5.9	35	1	FLAV_NOSSM	P35707	nostoc sp.
677	2	5.9	35	1	GBGU_MOUSE	Q61017	mus musculu
678	2	5.9	35	1	GRDB_CLOPU	P55793	clostridium
679	2	5.9	35	1	GUR_GYMSY	P25810	gymnema syl
680	2	5.9	35	1	HMWC_DESGI	P38588	desulfovibr
681	2	5.9	35	1	IAAC_HORVU	P34951	hordeum vul
682	2	5.9	35	1	KPPR_PINPS	P81664	pinus pinas
683	2	5.9	35	1	LCGB_LACLA	P36962	lactococcus
684	2	5.9	35	1	PBP1_LYMDI	P34176	lymantria d
685	2	5.9	35	1	PBP2_LYMDI	P34177	lymantria d
686	2	5.9	35	1	PBP_HYACE	P34175	hyalophora
687	2	5.9	35	1	PHI1_MYTCA	P35422	mytilus cal
688	2	5.9	35	1	PSAI_CYAPA	P48116	cyanophora
689	2	5.9	35	1	PSBT_MARPO	P12182	marchantia
690	2	5.9	35	1	PSBT_OENHO	P37258	oenothera h
691	2	5.9	35	1	PSBT_ORYSA	P12183	oryza sativ
692	2	5.9	35	1	PSBT_PINTH	P41625	pinus thunb
693	2	5.9	35	1	PSPC_PIG	P15785	sus scrofa
694	2	5.9	35	1	RL32_HALCU	P05965	halobacteri
695	2	5.9	35	1	SCKB_PANIM	P55928	pandinus im
696	2	5.9	35	1	SCKG_PANIM	Q10726	pandinus im
697	2	5.9	35	1	SCX1_BUTSI	P15229	buthus sind
698	2	5.9	35	1	SCX5_BUTEU	P15222	buthus eupe
699	2	5.9	35	1	SCXP_ANDMA	P01498	androctonus
700	2	5.9	35	1	SMS_LAMFL	Q9prro	lampetra fl
701	2	5.9	35	1	SPRC_PIG	P20112	sus scrofa

702	2	5.9	35	1	THPA_THADA	P21381	thaumatococ
703	2	5.9	35	1	TMTX_MESTA	Q9bn12	mesobuthus
704	2	5.9	35	1	TXAG_AGEOP	P31328	agelena opu
705	2	5.9	35	1	TXH4_SELHU	P83303	selenocosmi
706	2	5.9	35	1	TXKS_STOHE	P29187	stoichactis
707	2	5.9	35	1	TXN4_SELHA	P83471	selenocosmi
708	2	5.9	35	1	VL3_PAPVD	P06919	deer papill
709	2	5.9	35	1	VSPA_CERVI	P18692	cerastes vi
710	2	5.9	35	1	WSP7_PINPS	P81086	pinus pinas
711	2	5.9	35	1	Y320_BORBU	O51299	borrelia bu
712	2	5.9	35	1	Y37_BPT3	P20325	bacteriopha
713	2	5.9	35	1	Y644_ARCFU	O29613	archaeoglob
714	2	5.9	35	1	Y845_BORBU	O51785	borrelia bu
715	2	5.9	35	1	Y847_BORBU	O51787	borrelia bu
716	2	5.9	35	1	YC12_CYACA	Q9tlx0	cyanidium c
717	2	5.9	35	1	YC69_ARCFU	O28999	archaeoglob
718	2	5.9	35	1	YQB5_CAEEL	Q09258	caenorhabdi
719	2	5.9	36	1	AMPL_PIG	P28839	sus scrofa
720	2	5.9	36	1	ANFV_ANGJA	P22642	anguilla ja
721	2	5.9	36	1	C3L1_BOVIN	P30922	bos taurus
722	2	5.9	36	1	CBBA_NITVU	P37102	nitrobacter
723	2	5.9	36	1	CECD_ANTPE	P01511	antheraea p
724	2	5.9	36	1	CYC7_GEOME	P81894	geobacter m
725	2	5.9	36	1	DESR_DESGI	P00273	desulfovibr
726	2	5.9	36	1	F4RE_METOG	P80951	methanogeni
727	2	5.9	36	1	GLU1_ORENI	P81026	oreochromis
728	2	5.9	36	1	GLUC_HYDCO	P09682	hydrolagus
729	2	5.9	36	1	H1L5_ENSMI	P27203	ensis minor
730	2	5.9	36	1	HBB_PONPY	Q9tt34	pongo pygma
731	2	5.9	36	1	IAA_STRAU	P04082	streptomyce
732	2	5.9	36	1	IOB1_ISYOB	P58609	isyndus obs
733	2	5.9	36	1	KAD_STRGR	P53398	streptomyce
734	2	5.9	36	1	LHG_RHOVI	P04126	rhodopseudo
735	2	5.9	36	1	LYOX_PIG	P45845	sus scrofa
736	2	5.9	36	1	MFA1_YEAST	P34165	saccharomyc
737	2	5.9	36	1	MPG2_DACGL	Q41183	dactylis gl
738	2	5.9	36	1	MYPC_RAT	P56741	rattus norv
739	2	5.9	36	1	NEUH_CARCA	P11975	cardisoma c
740	2	5.9	36	1	NEUY_GADMO	P80167	gadus morhu
741	2	5.9	36	1	NEUY_ONCMY	P29071	oncorhynchu
742	2	5.9	36	1	NEUY_RABIT	P09640	oryctolagus
743	2	5.9	36	1	NEUY_RANRI	P29949	rana ridibu
744	2	5.9	36	1	NIFH_ENTAG	P26249	enterobacte
745	2	5.9	36	1	NLTP_PINPI	P26912	pinus pinea
746	2	5.9	36	1	NUCM_SOLTU	P80264	solanum tub
747	2	5.9	36	1	OST2_CHICK	P80897	gallus gall
748	2	5.9	36	1	PAHO_ALLMI	P06305	alligator m
749	2	5.9	36	1	PAHO_ANSAN	P06304	anser anser
750	2	5.9	36	1	PAHO_CERSI	P37999	ceratotheri
751	2	5.9	36	1	PAHO_DIDMA	P18107	didelphis m
752	2	5.9	36	1	PAHO_EQUZE	P38000	equus zebra
753	2	5.9	36	1	PAHO_ERIEU	P41335	erinaceus e
754	2	5.9	36	1	PAHO_LARAR	P41337	larus argen
755	2	5.9	36	1	PAHO_MACMU	P33684	macaca mula
756	2	5.9	36	1	PAHO_RABIT	P41336	oryctolagus
757	2	5.9	36	1	PAHO_RANCA	P15427	rana catesb
758	2	5.9	36	1	PAHO_RANTE	P31229	rana tempor

759	2	5.9	36	1	PAHO_STRCA	P11967	struthio ca
760	2	5.9	36	1	PAHO_TAPPI	P39659	tapirus pin
761	2	5.9	36	1	PGKH_CHLFU	P36232	chlorella f
762	2	5.9	36	1	PMY_PETMA	P80024	petromyzon
763	2	5.9	36	1	PSAD_PEA	P20117	pisum sativ
764	2	5.9	36	1	PSAH_PEA	P20121	pisum sativ
765	2	5.9	36	1	PSAI_ANGLY	P28251	angiopteris
766	2	5.9	36	1	PSAI_BRAOL	Q31909	brassica ol
767	2	5.9	36	1	PSAI_CARCL	Q9gdv2	carpobrotus
768	2	5.9	36	1	PSAI_CHAGL	Q8m9x5	chaetosphae
769	2	5.9	36	1	PSAI_CHLVU	P58214	chlorella v
770	2	5.9	36	1	PSAI_CYACA	Q9tm24	cyanidium c
771	2	5.9	36	1	PSAI_GUIITH	O78462	guillardia
772	2	5.9	36	1	PSAI_HORVU	P13165	hordeum vul
773	2	5.9	36	1	PSAI_MAIZE	P30980	zea mays (m
774	2	5.9	36	1	PSAI_MARPO	P12185	marchantia
775	2	5.9	36	1	PSAI_MESVI	Q9muq4	mesostigma
776	2	5.9	36	1	PSAI_NEPOL	Q9tl12	nephroselmi
777	2	5.9	36	1	PSAI_ORYSA	P12186	oryza sativ
778	2	5.9	36	1	PSAI_PICAB	O47040	picea abies
779	2	5.9	36	1	PSAI_PORPU	P51387	porphyra pu
780	2	5.9	36	1	PSAI_PSINU	Q8wil0	psilotum nu
781	2	5.9	36	1	PSAI_SKECO	O96813	skeletonema
782	2	5.9	36	1	PSAI_TOBAC	P12187	nicotiana t
783	2	5.9	36	1	PSAI_WHEAT	P25410	triticum ae
784	2	5.9	36	1	PSBI_ARATH	P09970	arabidopsis
785	2	5.9	36	1	PSBI_HORVU	P25876	hordeum vul
786	2	5.9	36	1	PSBI_MARPO	P09969	marchantia
787	2	5.9	36	1	PSBI_ORYSA	P12161	oryza sativ
788	2	5.9	36	1	PSBI_PINTH	P41599	pinus thunb
789	2	5.9	36	1	PSBI_PSEMZ	P29796	pseudotsuga
790	2	5.9	36	1	PSBM_CHLVU	P56325	chlorella v
791	2	5.9	36	1	PSBM_SYNEL	Q8dha7	synechococc
792	2	5.9	36	1	PSBY_ODOSI	P49543	odontella s
793	2	5.9	36	1	PSBY_PORPU	P51206	porphyra pu
794	2	5.9	36	1	PYY_AMICA	P29205	amia calva
795	2	5.9	36	1	PYY_LEPSP	P09473	lepisosteus
796	2	5.9	36	1	PYY_MYOSC	P09641	myoxocephal
797	2	5.9	36	1	PYY_ONCKI	P09474	oncorhynchu
798	2	5.9	36	1	PYY_ORENI	P81028	oreochromis
799	2	5.9	36	1	PYY_PIG	P01305	sus scrofa
800	2	5.9	36	1	PYY_RAJRH	P29206	raja rhina
801	2	5.9	36	1	PYY_RANRI	P29204	rana ridibu
802	2	5.9	36	1	SCK2_CENLL	P45630	centruroide
803	2	5.9	36	1	SCK3_LEIQH	P45660	leiurus qui
804	2	5.9	36	1	SCX1_BUTEU	P15220	buthus eupe
805	2	5.9	36	1	SCXL_LEIQU	P45639	leiurus qui
806	2	5.9	36	1	SPYY_PHYBI	P80952	phyllomedus
807	2	5.9	36	1	TAEK_ACTEQ	P81897	actinia equ
808	2	5.9	36	1	TERN_PSEUS	P82321	pseudacanth
809	2	5.9	36	1	TLN1_CHICK	P54939	gallus gall
810	2	5.9	36	1	TX35_PHONI	P81791	phoneutria
811	2	5.9	36	1	TXAM_METSE	P11495	metridium s
812	2	5.9	36	1	TXD3_PARLU	P83258	paracoelote
813	2	5.9	36	1	TXJA_HADVE	P82227	hadronyche
814	2	5.9	36	1	TXJB_HADVE	P82226	hadronyche
815	2	5.9	36	1	Y16L_BPT4	P39244	bacterioph

816	2	5.9	36	1	Y297_ARCFU	029945	archaeoglob
817	2	5.9	36	1	Y4KD_BPCHP	P19188	bacterioph
818	2	5.9	36	1	Y609_ARCFU	029646	archaeoglob
819	2	5.9	36	1	Y609_BORBU	051554	borrelia bu
820	2	5.9	36	1	Y619_ARCFU	029636	archaeoglob
821	2	5.9	36	1	Y699_TREPA	083697	treponema p
822	2	5.9	36	1	YC12_CYAPA	P48256	cyanophora
823	2	5.9	36	1	YG50_HAEIN	P44281	haemophilus
824	2	5.9	36	1	YRKG_BACSU	P54434	bacillus su
825	2	5.9	37	1	24KD_PLACH	P14592	plasmodium
826	2	5.9	37	1	AFP4_MALPA	P83138	malva parvi
827	2	5.9	37	1	ANP3_PSEAM	P02733	pseudopleur
828	2	5.9	37	1	ATPO_SOLTU	P80504	solanum tub
829	2	5.9	37	1	B2MG_ORENI	Q03423	oreochromis
830	2	5.9	37	1	CAL1_PIG	P30880	sus scrofa
831	2	5.9	37	1	CAL1_SHEEP	P30881	ovis aries
832	2	5.9	37	1	CALR_RANRI	P31888	rana ridibu
833	2	5.9	37	1	CEC2_MANSE	P14662	manduca sex
834	2	5.9	37	1	CEC3_MANSE	P14663	manduca sex
835	2	5.9	37	1	CEC4_MANSE	P14664	manduca sex
836	2	5.9	37	1	CG2S_LUPAN	P09930	lupinus ang
837	2	5.9	37	1	CHCD_ANTPO	P08931	antheraea p
838	2	5.9	37	1	CS40_STAAU	P81684	staphylococ
839	2	5.9	37	1	CUP4_SARBU	P14486	sarcophaga
840	2	5.9	37	1	DEF4_ANDAU	P56686	androctonus
841	2	5.9	37	1	DEFA_MYTED	P81610	mytilus edu
842	2	5.9	37	1	ECAA_ECTTU	P49343	ectatomma t
843	2	5.9	37	1	ES2A_RANES	P40845	rana escule
844	2	5.9	37	1	ES2B_RANES	P40846	rana escule
845	2	5.9	37	1	F13A_BOVIN	P12260	bos taurus
846	2	5.9	37	1	GHR3_RAT	P33580	rattus norv
847	2	5.9	37	1	HCYB_CANPG	P83175	cancer pagu
848	2	5.9	37	1	HOXF_RHOOP	P22658	rhodococcus
849	2	5.9	37	1	LPPY_SERMA	P19937	serratia ma
850	2	5.9	37	1	MAUR_PARVE	Q56462	paracoccus
851	2	5.9	37	1	ME20_EUPRA	P26888	euplotes ra
852	2	5.9	37	1	ME22_EUPRA	P58548	euplotes ra
853	2	5.9	37	1	MIBP_PSESP	P04576	pseudomonas
854	2	5.9	37	1	NLT3_VITSX	P80273	vitis sp. (
855	2	5.9	37	1	NLT4_VITSX	P80274	vitis sp. (
856	2	5.9	37	1	NUFM_SOLTU	P80266	solanum tub
857	2	5.9	37	1	OP2A_OXYKI	P83248	oxyopes kit
858	2	5.9	37	1	OP2B_OXYKI	P83249	oxyopes kit
859	2	5.9	37	1	OP2C_OXYKI	P83250	oxyopes kit
860	2	5.9	37	1	OP2D_OXYKI	P83251	oxyopes kit
861	2	5.9	37	1	PETG_ANASP	P58246	anabaena sp
862	2	5.9	37	1	PETG_ANAVA	Q913p7	anabaena va
863	2	5.9	37	1	PETG_ARATH	P56775	arabidopsis
864	2	5.9	37	1	PETG_CHAGL	Q8m9y4	chaetosphae
865	2	5.9	37	1	PETG_CHLEU	P46304	chlamydomon
866	2	5.9	37	1	PETG_CHLRE	Q08362	chlamydomon
867	2	5.9	37	1	PETG_CHLVU	P56305	chlorella v
868	2	5.9	37	1	PETG_CUSRE	P30398	cuscuta ref
869	2	5.9	37	1	PETG_CYAPA	P14236	cyanophora
870	2	5.9	37	1	PETG_EUGGR	P30396	euglena gra
871	2	5.9	37	1	PETG_GUITH	O78505	guillardia
872	2	5.9	37	1	PETG_MARPO	P12120	marchantia

873	2	5.9	37	1	PETG_MESVI	Q9mun3	mesostigma
874	2	5.9	37	1	PETG_NEPOL	Q9tky8	nephroselmi
875	2	5.9	37	1	PETG_ODOSI	P49470	odontella s
876	2	5.9	37	1	PETG_ORYSA	P12121	oryza sativ
877	2	5.9	37	1	PETG_PINTH	P41614	pinus thunb
878	2	5.9	37	1	PETG_PORPU	P51318	porphyra pu
879	2	5.9	37	1	PETG_PSINU	Q8wi02	psilotum nu
880	2	5.9	37	1	PETG_SKECO	O96811	skeletonema
881	2	5.9	37	1	PETG_SYNEL	Q8dki2	synechococc
882	2	5.9	37	1	PETG_SYN7	Q9z3g1	synechococc
883	2	5.9	37	1	PIIL_ACHLY	P81720	achromobact
884	2	5.9	37	1	POLN_WEEV	P13896	western equ
885	2	5.9	37	1	PRF1_RAT	P18889	rattus norv
886	2	5.9	37	1	PRT3_SCYCA	P30258	scyliorhinu
887	2	5.9	37	1	PSAI_ARATH	P56768	arabidopsis
888	2	5.9	37	1	PSAJ_EUGGR	P30394	euglena gra
889	2	5.9	37	1	PSBL_ARATH	P29301	arabidopsis
890	2	5.9	37	1	PSBL_ORYSA	P12166	oryza sativ
891	2	5.9	37	1	PSBY_CYACA	O19893	cyanidium c
892	2	5.9	37	1	PSBY_GUIITH	O78433	guillardia
893	2	5.9	37	1	PYY_CHICK	P29203	gallus gall
894	2	5.9	37	1	REV_SIVM2	P08809	simian immu
895	2	5.9	37	1	RK36_ARATH	P12144	arabidopsis
896	2	5.9	37	1	RK36_ASTLO	P24355	astasia lon
897	2	5.9	37	1	RK36_CHLVU	P56360	chlorella v
898	2	5.9	37	1	RK36_CYACA	Q9tlu9	cyanidium c
899	2	5.9	37	1	RK36_CYAPA	P48131	cyanophora
900	2	5.9	37	1	RK36_EPIVI	P30069	epifagus vi
901	2	5.9	37	1	RK36_EUGGR	P21532	euglena gra
902	2	5.9	37	1	RK36_LOTJA	Q9bbq2	lotus japon
903	2	5.9	37	1	RK36_MARPO	P12142	marchantia
904	2	5.9	37	1	RK36_NEPOL	Q9tl26	nephroselmi
905	2	5.9	37	1	RK36_ODOSI	P49568	odontella s
906	2	5.9	37	1	RK36_OENHO	Q9mtj1	oenothera h
907	2	5.9	37	1	RK36_ORYSA	P12143	oryza sativ
908	2	5.9	37	1	RK36_PEA	P07815	pisum sativ
909	2	5.9	37	1	RK36_PINTH	P41631	pinus thunb
910	2	5.9	37	1	RK36_PORPU	P51296	porphyra pu
911	2	5.9	37	1	RK36_PSINU	Q8why9	psilotum nu
912	2	5.9	37	1	RK36_SPIOL	P12230	spinacia ol
913	2	5.9	37	1	RL36_ANASP	Q8ypk0	anabaena sp
914	2	5.9	37	1	RL36_AQUAE	O66487	aquifex aeo
915	2	5.9	37	1	RL36_BACHD	O50631	bacillus ha
916	2	5.9	37	1	RL36_BACST	P07841	bacillus st
917	2	5.9	37	1	RL36_BACSU	P20278	bacillus su
918	2	5.9	37	1	RL36_BORBU	O51452	borrelia bu
919	2	5.9	37	1	RL36_CAMJE	Q9pm84	campylobact
920	2	5.9	37	1	RL36_CLOAB	Q97ek2	clostridium
921	2	5.9	37	1	RL36_CLOPE	Q8xhu7	clostridium
922	2	5.9	37	1	RL36_DEIRA	Q9rsk0	deinococcus
923	2	5.9	37	1	RL36_HAEIN	P46361	haemophilus
924	2	5.9	37	1	RL36_HELPJ	Q9zjt1	helicobacte
925	2	5.9	37	1	RL36_HELPY	P56058	helicobacte
926	2	5.9	37	1	RL36_LEPIN	Q9xd13	leptospira
927	2	5.9	37	1	RL36_LISMO	Q927n0	listeria mo
928	2	5.9	37	1	RL36_MYCGA	Q9rdv9	mycoplasma
929	2	5.9	37	1	RL36_MYCGE	P47420	mycoplasma

930	2	5.9	37	1	RL36_MYCPN	P52864	mycoplasma
931	2	5.9	37	1	RL36_MYCPU	Q98q05	mycoplasma
932	2	5.9	37	1	RL36_MYCSP	P38015	mycoplasma
933	2	5.9	37	1	RL36_MYCTU	P45810	mycobacteri
934	2	5.9	37	1	RL36_NEIMA	Q9jrb2	neisseria m
935	2	5.9	37	1	RL36_STAAM	Q99s42	staphylococ
936	2	5.9	37	1	RL36_STRCO	O86772	streptomyce
937	2	5.9	37	1	RL36_SYNP6	O24707	synechococc
938	2	5.9	37	1	RL36_THETH	P80256	thermus the
939	2	5.9	37	1	RL36_THETN	Q8r7x8	thermoanaer
940	2	5.9	37	1	RL36_TREPA	O83239	treponema p
941	2	5.9	37	1	RL36_UREPA	Q9pqn7	ureaplasma
942	2	5.9	37	1	RL36_VIBCH	P78001	vibrio chol
943	2	5.9	37	1	RL7_CLOPA	P05393	clostridium
944	2	5.9	37	1	RS15_HELLU	P52820	helix lucor
945	2	5.9	37	1	RUGC_RANRU	P80956	rana rugosa
946	2	5.9	37	1	SCIT_MESTA	P81761	mesobuthus
947	2	5.9	37	1	SCK2_LEIQH	P45628	leiurus qui
948	2	5.9	37	1	SCK3_BUTOC	P59290	buthus occi
949	2	5.9	37	1	SCK3_PARTR	P83112	parabuthus
950	2	5.9	37	1	SCKA_TITSE	P46114	tityus serr
951	2	5.9	37	1	SCKC_LEIQH	P13487	leiurus qui
952	2	5.9	37	1	SMS_PETMA	P21779	petromyzon
953	2	5.9	37	1	TCTP_TRYBB	P35758	trypanosoma
954	2	5.9	37	1	THHS_HORVU	P33045	hordeum vul
955	2	5.9	37	1	TX21_SELHU	P82959	selenocosmi
956	2	5.9	37	1	TX22_SELHU	P82960	selenocosmi
957	2	5.9	37	1	TXD1_PARLU	P83256	paracoelote
958	2	5.9	37	1	TXD2_PARLU	P83257	paracoelote
959	2	5.9	37	1	TXD4_PARLU	P83259	paracoelote
960	2	5.9	37	1	TXJC_HADVE	P82228	hadronyche
961	2	5.9	37	1	TXKB_BUNGR	P29186	bunodosoma
962	2	5.9	37	1	TXOF_HADVE	P81599	hadronyche
963	2	5.9	37	1	TXP3_APTSC	P49268	aptostichus
964	2	5.9	37	1	VA1_BPBF2	P19347	bacterioph
965	2	5.9	37	1	VG40_BPML5	Q05250	mycobacteri
966	2	5.9	37	1	VG65_BPPH2	P16515	bacterioph
967	2	5.9	37	1	VG65_BPPZA	P08384	bacterioph
968	2	5.9	37	1	VGJ_BPPHX	P03651	bacterioph
969	2	5.9	37	1	VP64_NPVBM	P41722	bombyx mori
970	2	5.9	37	1	VPU_HV1Z8	P08807	human immun
971	2	5.9	37	1	Y268_ARCFU	O29971	archaeoglob
972	2	5.9	37	1	Y63_BPT7	P03799	bacterioph
973	2	5.9	37	1	Y692_BORBU	O51635	borrelia bu
974	2	5.9	37	1	Y700_BORBU	O51643	borrelia bu
975	2	5.9	37	1	Y762_BORBU	O51703	borrelia bu
976	2	5.9	37	1	Y846_BORBU	O51786	borrelia bu
977	2	5.9	37	1	YBGT_ECOLI	P56100	escherichia
978	2	5.9	37	1	YC12_CHLVU	P56328	chlorella v
979	2	5.9	37	1	YDA3_SCHPO	Q10345	schizosacch
980	2	5.9	37	1	YQGE_BACCA	P28753	bacillus ca
981	2	5.9	37	1	YRYL_CAEEL	Q19177	caenorhabdi
982	2	5.9	38	1	A2M_HOMAM	P20737	homarus ame
983	2	5.9	38	1	AFP5_MALPA	P83139	malva parvi
984	2	5.9	38	1	BD01_BOVIN	P46159	bos taurus
985	2	5.9	38	1	BD08_BOVIN	P46166	bos taurus
986	2	5.9	38	1	BD11_BOVIN	P46169	bos taurus

987	2	5.9	38	1	BD12_BOVIN	P46170	bos taurus
988	2	5.9	38	1	COA3_XANCP	Q07484	xanthomonas
989	2	5.9	38	1	CPRP_CANPG	P81033	cancer pagu
990	2	5.9	38	1	CRS3_NOTGO	P15534	nototodarus
991	2	5.9	38	1	CU47_LACCU	P80323	lactobacill
992	2	5.9	38	1	DCHS_MICSP	P00863	micrococcus
993	2	5.9	38	1	DEF4_LEIQH	P41965	leiurus qui
994	2	5.9	38	1	DEF7_SPIOL	P81573	spinacia ol
995	2	5.9	38	1	DEFI_AESCY	P80154	aeschna cya
996	2	5.9	38	1	DEFI_MYTGA	P80571	mytilus gal
997	2	5.9	38	1	DLP3_ORNAN	P82141	ornithorhyn
998	2	5.9	38	1	DPOB_BOVIN	Q27958	bos taurus
999	2	5.9	38	1	E2F1_RAT	O09139	rattus norv
1000	2	5.9	38	1	EST5_DROMO	P10095	drosophila

ALIGNMENTS

RESULT 1

FABI_RHASA

ID FABI_RHASA STANDARD; PRT; 33 AA.

AC P81175;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Fatty acid-binding protein, intestinal (I-FABP) (FABPI) (Fragments).

OS Rhamdia sapo.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;

OC Pimelodidae; Rhamdia.

OX NCBI_TaxID=55673;

RN [1]

RP SEQUENCE.

RC TISSUE=Intestine;

RX MEDLINE=98036128; PubMed=9370361;

RA Di Pietro S.M., Dell'Angelica E.C., Veerkamp J.H., Sterin-Speziale N.,

RA Santome J.A.;

RT "Amino acid sequence, binding properties and evolutionary

RT relationships of the basic liver fatty-acid-binding protein from the

RT catfish Rhamdia sapo.";

RL Eur. J. Biochem. 249:510-517(1997).

CC -!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR

CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- TISSUE SPECIFICITY: INTESTINE.

CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF

CC TRANSPORTERS.

DR InterPro; IPR000463; Fatty_acid_BP.

DR PROSITE; PS00214; FABP; PARTIAL.

KW Transport; Lipid-binding.

FT NON_TER 1 1

FT NON_CONS 12 13

FT NON_CONS 20 21

FT NON_CONS 28 29

FT NON_TER 33 33

SQ SEQUENCE 33 AA; 3660 MW; 5BA16CC2880B7819 CRC64;

Query Match 14.7%; Score 5; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
|||||
Db 13 SVSEI 17

RESULT 2

DMD_RAT

ID DMD_RAT STANDARD; PRT; 29 AA.
AC P11530;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dystrophin (Fragment).
GN DMD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122671; PubMed=3340214;
RA Nudel U., Robzyk K., Yaffe D.;
RT "Expression of the putative Duchenne muscular dystrophy gene in
RT differentiated myogenic cell cultures and in the brain.";
RL Nature 331:635-638(1988).
CC -!- FUNCTION: May play a role in anchoring the cytoskeleton to the
CC plasma membrane.
CC -!- SUBUNIT: Interacts with the syntrophins SNTA1, SNTB1, SNTB2, SNTG1
CC and SNTG2 (By similarity).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07000; CAA30057.1; -.
DR PIR; S01614; S01614.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR PROSITE; PS00019; ACTININ_1; PARTIAL.
DR PROSITE; PS00020; ACTININ_2; PARTIAL.
DR PROSITE; PS01159; WW_DOMAIN_1; PARTIAL.
DR PROSITE; PS50020; WW_DOMAIN_2; PARTIAL.
KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
KW Repeat.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3289 MW; 8ECFB28A1A7ACAF0 CRC64;

Query Match 11.8%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
||||
Db 12 KLQD 15

RESULT 3

ANF_RANRI

ID ANF_RANRI STANDARD; PRT; 30 AA.
AC P09196;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Atrial natriuretic factor (ANF) (Atrial natriuretic peptide) (ANP).
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart atrium;
RX MEDLINE=89005705; PubMed=2971573;
RA Lazure C., Ong H., McNicoll N., Netchitailo P., Chretien M.,
RA de Lean A., Vaudry H.;
RT "The amino acid sequences of frog heart atrial natriuretic-like
RT peptide and mammalian ANF are closely related.";
RL FEBS Lett. 238:300-306(1988).
CC -!- FUNCTION: VASOACTIVE ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
DR PIR; S01657; S01657.
DR InterPro; IPR002407; At_natriurtcpep.
DR InterPro; IPR000663; Natr_peptide.
DR Pfam; PF00212; ANP; 1.
DR PRINTS; PR00710; NATPEPTIDES.
DR ProDom; PD005107; At_natriurtcpep; 1.
DR SMART; SM00183; NAT_PEP; 1.
DR PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
KW Vasoactive.
FT DISULFID 11 27
SQ SEQUENCE 30 AA; 3263 MW; 175A946321C27DA0 CRC64;

Query Match 11.8%; Score 4; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SMRR 20
||||
Db 4 SMRR 7

RESULT 4

ERFK_KLEAE

ID ERFK_KLEAE STANDARD; PRT; 35 AA.

AC Q08599;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable protein erfK/srfK precursor (Fragment).
 GN ERFK.
 OS Klebsiella aerogenes.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=28451;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W70 / KC1043;
 RX MEDLINE=93209957; PubMed=8458853;
 RA Schwacha A., Bender R.A.;
 RT "The nac (nitrogen assimilation control) gene from Klebsiella
 RT aerogenes.";
 RL J. Bacteriol. 175:2107-2115(1993).
 CC -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
 CC -!- SIMILARITY: BELONGS TO THE ERFK/YBIS/YCFS/YNHG FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L01114; AAA18175.2; ALT_INIT.
 KW Periplasmic; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 >35 PROBABLE PROTEIN ERFK/SRFK.
 FT NON_TER 35 35
 SQ SEQUENCE 35 AA; 3721 MW; 785E30CCDEC2C763 CRC64;

Query Match 11.8%; Score 4; DB 1; Length 35;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MRRV 21
 ||||
 Db 1 MRRV 4

RESULT 5

PSBY_SYNY3

ID PSBY_SYNY3 STANDARD; PRT; 39 AA.
 AC P73676;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Photosystem II protein Y.
 GN PSBY OR SML0007.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugiura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions."
 RL DNA Res. 3:109-136(1996).
 CC !- FUNCTION: MANGANESE-BINDING POLYPEPTIDE WITH L-ARGININE
 CC METABOLIZING ENZYME ACTIVITY. COMPONENT OF THE CORE OF PHOTOSYSTEM
 CC II (BY SIMILARITY).
 CC !- SUBCELLULAR LOCATION: CELLULAR THYLAKOID MEMBRANE.
 CC !- SIMILARITY: BELONGS TO THE PSBY FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D90908; BAA17722.1; -.
 DR PIR; S77164; S77164.
 KW Photosystem II; Transmembrane; Thylakoid; Complete proteome.
 FT TRANSMEM 5 25 POTENTIAL.
 SQ SEQUENCE 39 AA; 4202 MW; 3EA176ABAA79F6DF CRC64;

Query Match 11.8%; Score 4; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQDV 31
 ||||
 Db 31 LQDV 34

RESULT 6

SR1C_SARPE

ID SR1C_SARPE STANDARD; PRT; 39 AA.
 AC P08377;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sarcotoxin IC.
 OS Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7386;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85207747; PubMed=3888997;

RA Okada M., Natori S.;
 RT "Primary structure of sarcotoxin I, an antibacterial protein induced
 RT in the hemolymph of *Sarcophaga peregrina* (flesh fly) larvae.";
 RL J. Biol. Chem. 260:7174-7177(1985).
 CC -!- FUNCTION: SARCOTOXINS, WHICH ARE POTENT BACTERICIDAL PROTEINS,
 CC ARE PRODUCED IN RESPONSE TO INJURY. THEY ARE CYTOTOXIC TO BOTH
 CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
 DR PIR; C22625; CKFHCS.
 DR InterPro; IPR000875; Cecropin.
 DR InterPro; IPR003253; Sarctxn_cecrpn.
 DR Pfam; PF00272; cecropin; 1.
 DR ProDom; PD001670; Sarctxn_cecrpn; 1.
 DR PROSITE; PS00268; CECROPIN; 1.
 KW Insect immunity; Antibiotic; Hemolymph; Amidation; Multigene family.
 FT MOD_RES 39 39 AMIDATION.
 SQ SEQUENCE 39 AA; 4227 MW; 11E79F4F405E855A CRC64;

Query Match 11.8%; Score 4; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
 ||||
 Db 2 WLRK 5

RESULT 7

CH60_MYCSM

ID CH60_MYCSM STANDARD; PRT; 28 AA.
 AC P80673;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Fragment).
 GN GROL OR GROEL OR MOPA.
 OS *Mycobacterium smegmatis*.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1772;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;
 RX MEDLINE=97387814; PubMed=9243799;
 RA Lundrigan M.D., Arceneaux J.E.L., Zhu W., Byers B.R.;
 RT "Enhanced hydrogen peroxide sensitivity and altered stress protein
 RT expression in iron-starved *Mycobacterium smegmatis*."
 RL BioMetals 10:215-225(1997).
 CC -!- FUNCTION: Prevents misfolding and promotes the refolding and
 CC proper assembly of unfolded polypeptides generated under stress
 CC conditions.
 CC -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
 CC 7 subunits (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
 DR HAMAP; MF_00600; -; 1.

DR InterPro; IPR001844; Chaprnin_Cpn60.
DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
KW Chaperone; ATP-binding.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3047 MW; 2F40F27B94EF8720 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 18 LNS 20

RESULT 8

COXB_SOLTU

ID COXB_SOLTU STANDARD; PRT; 28 AA.
AC P80499;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Vb (EC 1.9.3.1) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RC TISSUE=Tuber;
RX MEDLINE=97077345; PubMed=8919912;
RA Jansch L., Krufft V., Schmitz U.K., Braun H.P.;
RT "New insights into the composition, molecular mass and stoichiometry
RT of the protein complexes of plant mitochondria."
RL Plant J. 9:357-368(1996).
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.
DR InterPro; IPR002124; COX5B.
DR PROSITE; PS00848; COX5B; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3101 MW; 1EAFA79E2682849C CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSE 4
|||
Db 2 VSE 4

RESULT 9

GUN_SCHCO

ID GUN_SCHCO STANDARD; PRT; 28 AA.
AC P81190;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endoglucanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
DE (Fragment).
OS Schizophyllum commune (Bracket fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllaceae; Schizophyllum.
OX NCBI_TaxID=5334;
RN [1]
RP SEQUENCE.
RX MEDLINE=97459758; PubMed=9315718;
RA Clarke A.J., Drummelsmith J., Yaguchi M.;
RT "Identification of the catalytic nucleophile in the cellulase from
RT Schizophyllum commune and assignment of the enzyme to Family 5,
RT subtype 5 of the glycosidases.";
RL FEBS Lett. 414:359-361(1997).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC linkages in cellulose, lichenin and cereal beta-D-glucans.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Probable).
CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
CC HYDROLASES).
DR InterPro; IPR001547; Glyco_hydro_5.
DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; PARTIAL.
KW Cellulose degradation; Hydrolase; Glycosidase; Zymogen; Membrane;
KW Lipoprotein.
FT ACT_SITE 20 20 NUCLEOPHILE.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 2937 MW; B3F1C0C99C9950BE CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
|||
Db 7 EWL 9

RESULT 10

LPL_ECOLI

ID LPL_ECOLI STANDARD; PRT; 28 AA.
AC P09149; Q8VSS2; Q8VSS3;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu operon leader peptide.
GN LEUL OR LEULP OR B0075 OR C5492 OR Z0084 OR ECS0079 OR SF0070.
OS Escherichia coli,
OS Escherichia coli O6,
OS Escherichia coli O157:H7, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562, 217992, 83334, 623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12;
 RX MEDLINE=82078077; PubMed=6171647;
 RA Wessler S.R., Calvo J.M.;
 RT "Control of leu operon expression in Escherichia coli by a
 RT transcription attenuation mechanism.";
 RL J. Mol. Biol. 149:579-597(1981).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12;
 RX MEDLINE=92334977; PubMed=1630901;
 RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
 RA Isono K., Mizobuchi K., Nakata A.;
 RT "Systematic sequencing of the Escherichia coli genome: analysis of
 RT the 0-2.4 min region.";
 RL Nucleic Acids Res. 20:3305-3308(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=06:H1 / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 RT of uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533(2001).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 RN [7]
 RP SEQUENCE OF 1-19 FROM N.A.
 RC SPECIES=*E.coli*; STRAIN=O157:H7 / Au6, and O157:H7 / Au1808;
 RX MEDLINE=21555105; PubMed=11698378;
 RA Kim J., Nietfeldt J.W., Ju J., Wise J., Fegan N., Desmarchelier P.,
 RA Benson A.K.;
 RT "Ancestral divergence, genome diversification, and phylogeographic
 RT variation in subpopulations of sorbitol-negative, beta-glucuronidase-
 RT negative enterohemorrhagic *Escherichia coli* O157.";
 RL J. Bacteriol. 183:6885-6897(2001).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC SPECIES=*S.flexneri*; STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; PubMed=12384590;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity
 RT through comparison with genomes of *Escherichia coli* K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 CC -!- FUNCTION: Involved in control of the biosynthesis of leucine.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J01642; AAA24065.1; -.
 DR EMBL; X55034; CAA38852.1; -.
 DR EMBL; D10483; BAB96644.1; -.
 DR EMBL; AE000118; AAC73186.1; -.
 DR EMBL; AE016755; AAN78588.1; -.
 DR EMBL; AE005184; AAG54379.1; -.
 DR EMBL; AP002550; BAB33502.1; -.
 DR EMBL; AF368047; AAL38429.1; -.
 DR EMBL; AF368048; AAL38430.1; -.
 DR EMBL; AE015044; AAN41735.1; -.
 DR PIR; A30376; LFECL.
 DR PIR; G85489; G85489.
 DR PIR; G90638; G90638.
 DR EcoGene; EG11280; leuL.
 KW Leucine biosynthesis; Leader peptide; Complete proteome.
 FT VARIANT 13 13 L -> LL (IN STRAIN AU1808).
 SQ SEQUENCE 28 AA; 3146 MW; 63914DFFD94E122E CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 RRV 21
|||
Db 21 RRV 23

RESULT 11

PA23_TRIST

ID PA23_TRIST STANDARD; PRT; 28 AA.
AC P82894;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2, basic 3 (EC 3.1.1.4) (PA2-III) (PLA2-III)
DE (Phosphatidylcholine 2-acylhydrolase) (Fragment).
OS Trimeresurus stejnegeri (Chinese green tree viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=39682;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Li S.Y., Wang W.Y., Xiong Y.L.;
RT "Isolation, sequence and characterization of five variants of
RT phospholipase A2 from venom of snake Trimeresurus stejnegeri.";
RL Submitted (DEC-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides. Hemolytic and neurotoxic
CC activities are not detected.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP II
CC SUBFAMILY.
DR HSSP; P82287; 1QLL.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR PROSITE; PS00119; PA2_ASP; PARTIAL.
DR PROSITE; PS00118; PA2_HIS; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Multigene family.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3023 MW; 042104521CA1F103 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGK 13
|||
Db 5 LGK 7

RESULT 12

PA2C_PSEPO

ID PA2C_PSEPO STANDARD; PRT; 28 AA.
AC P20260;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Pseudexin C chain) (Phosphatidylcholine
DE 2-acylhydrolase) (Fragment).
OS Pseudechis porphyriacus (Red-bellied black snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudechis.
OX NCBI_TaxID=8671;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=89388835; PubMed=2675391;
RA Schmidt J.J., Middlebrook J.L.;
RT "Purification, sequencing and characterization of pseudexin
RT phospholipases A2 from Pseudechis porphyriacus (Australian
RT red-bellied black snake).";
RL Toxicon 27:805-818(1989).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I
CC SUBFAMILY.
DR PIR; C32416; C32416.
DR HSSP; P00592; 2PHI.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR PROSITE; PS00119; PA2_ASP; PARTIAL.
DR PROSITE; PS00118; PA2_HIS; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Multigene family.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3210 MW; 5089A7E85CAA0D5 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7
|||
Db 3 IQL 5

RESULT 13

VI03_VACCP

ID VI03_VACCP STANDARD; PRT; 28 AA.
AC Q00334;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)

DE Protein I3 (Fragment).
 GN I3L.
 OS Vaccinia virus (strain L-IVP).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=31531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91066899; PubMed=2250685;
 RA Ryazankina O.I., Shchelkunov S.N., Muravlev A.I., Netesova N.A.,
 RA Mikryukov N.N., Gutorov V.V., Nikulin A.E., Kulichkov V.A.,
 RA Malygin E.G.;
 RT "Molecular-biological study of vaccinia virus genome. II.
 RT Localization and nucleotide sequence of vaccinia virus genes coding
 RT for proteins 36K and 12K.";
 RL Mol. Biol. (Mosk) 24:968-976(1990).
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED IN THE EARLY AS WELL AS
 CC THE LATE PHASE OF INFECTION.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X61165; CAA43473.1; -.
 DR InterPro; IPR006754; Pox_I3.
 DR Pfam; PF04661; Pox_I3; 1.
 KW Early protein; Late protein.
 FT NON_TER 1 1
 SQ SEQUENCE 28 AA; 3238 MW; CE10813AC544F010 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
 |||
 Db 5 NLG 7

RESULT 14

VIP_ALLMI

ID VIP_ALLMI STANDARD; PRT; 28 AA.
 AC P48142; P01285;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 GN VIP.
 OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]

RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=93324451; PubMed=8101369;
RA Wang Y., Conlon J.M.;
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
RT and stomach of the alligator.";
RL Peptides 14:573-579(1993).
CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
CC AND GALL BLADDER.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Amidation; Hormone.
FT MOD_RES 28 28 AMIDATION.
SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 15

VIP_RANRI
ID VIP_RANRI STANDARD; PRT; 28 AA.
AC P81016;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Vasoactive intestinal peptide (VIP).
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RX MEDLINE=95309202; PubMed=7540547;
RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
RT "Frog vasoactive intestinal polypeptide and galanin: primary
RT structures and effects on pituitary adenylate cyclase.";
RL Endocrinology 136:3079-3086(1995).
CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
CC AND GALL BLADDER.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.

DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Amidation; Hormone.
FT MOD_RES 28 28 AMIDATION.
SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 16

VIP_SHEEP

ID VIP_SHEEP STANDARD; PRT; 28 AA.
AC P04565;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Vasoactive intestinal peptide (VIP).
GN VIP.
OS Ovis aries (Sheep),
OS Capra hircus (Goat), and
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940, 9925, 9615;
RN [1]
RP SEQUENCE.
RC SPECIES=Sheep; TISSUE=Brain;
RX MEDLINE=91045331; PubMed=2235680;
RA Gafvelin G.;
RT "Isolation and primary structure of VIP from sheep brain.";
RL Peptides 11:703-706(1990).
RN [2]
RP SEQUENCE.
RC SPECIES=Sheep; TISSUE=Small intestine;
RX MEDLINE=91239834; PubMed=2034821;
RA Bounjoua Y., Vandermeers A., Robberecht P., Vandermeers-Piret M.C.,
RA Christophe J.;
RT "Purification and amino acid sequence of vasoactive intestinal
RT peptide, peptide histidine isoleucinamide and secretin from the ovine
RT small intestine.";
RL Regul. Pept. 32:169-179(1991).
RN [3]
RP SEQUENCE.
RC SPECIES=C.hircus, and C.familiaris;
RX MEDLINE=86313167; PubMed=3748846;
RA Eng J., Du B.-H., Raufman J.-P., Yalow R.S.;
RT "Purification and amino acid sequences of dog, goat and guinea pig
RT VIPs.";
RL Peptides 7 Suppl. 1:17-20(1986).
CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES

CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; A60304; A60304.
 DR PIR; B60072; VRSH.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3327 MW; EF313FB573FF6F3F CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 17

GALA_ALLMI

ID GALA_ALLMI STANDARD; PRT; 29 AA.
 AC P47215;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95023390; PubMed=7524049;
 RA Wang Y., Conlon J.M.;
 RT "Purification and primary structure of galanin from the alligator
 RT stomach."
 RL Peptides 15:603-606(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3216 MW; E02F019B2D3E0529 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 18

GALA_AMICA

ID GALA_AMICA STANDARD; PRT; 29 AA.
AC P47214;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
OS Amia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Amiiformes; Amiidae; Amia.
OX NCBI_TaxID=7924;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=95083480; PubMed=7527531;
RA Wang Y., Conlon J.M.;
RT "Purification and characterization of galanin from the
RT phylogenetically ancient fish, the bowfin (*Amia calva*) and dogfish
RT (*Scyliorhinus canicula*).";
RL Peptides 15:981-986(1994).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3114 MW; 7518719B2D271627 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 19

GALA_CHICK

ID GALA_CHICK STANDARD; PRT; 29 AA.
AC P30802;

DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 GN GAL OR GALN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=91348254; PubMed=1715289;
 RA Norberg A., Sillard R., Carlquist M., Joernvall H., Mutt V.;
 RT "Chemical detection of natural peptides by specific structures.
 RT Isolation of chicken galanin by monitoring for its N-terminal
 RT dipeptide, and determination of the amino acid sequence.";
 RL FEBS Lett. 288:151-153(1991).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR PIR; S17147; S17147.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR PRINTS; PR00273; GALANIN.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3212 MW; EB66919B2D271629 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 20

GALA_ONCMY

ID GALA_ONCMY STANDARD; PRT; 29 AA.
 AC P47213;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;

RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95164756; PubMed=7532194;
 RA Anglade I., Wang Y., Jensen J., Tramu G., Kah O., Conlon J.M.;
 RT "Characterization of trout galanin and its distribution in trout
 RT brain and pituitary.";
 RL J. Comp. Neurol. 350:63-74(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3044 MW; 73C37190403FA349 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 21

GALA_RANRI

ID GALA_RANRI STANDARD; PRT; 29 AA.
 AC P47216;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95309202; PubMed=7540547;
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
 RT "Frog vasoactive intestinal polypeptide and galanin: primary
 RT structures and effects on pituitary adenylate cyclase.";
 RL Endocrinology 136:3079-3086(1995).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.

DR Pfam; PF01296; Galanin; 1.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3162 MW; F718719B2D3FB529 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 22

GALA_SHEEP

ID GALA_SHEEP STANDARD; PRT; 29 AA.
AC P31234;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
GN GAL OR GALN OR GLNN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92158824; PubMed=1724081;
RA Sillard R., Langel U., Joernvall H.;
RT "Isolation and characterization of galanin from sheep brain.";
RL Peptides 12:855-859(1991).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR PRINTS; PR00273; GALANIN.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3185 MW; F718719B2D3FB089 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17

Db |||
 4 LNS 6

RESULT 23

GLUC_CHIBR

ID GLUC_CHIBR STANDARD; PRT; 29 AA.
AC P31297;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucagon.
GN GCG.
OS Chinchilla brevicaudata (Chinchilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Chinchillidae;
OC Chinchilla.
OX NCBI_TaxID=10152;
RN [1]
RP SEQUENCE.
RX MEDLINE=91045327; PubMed=2235678;
RA Eng J., Kleinman W.A., Chu L.S.;
RT "Purification of peptide hormones from chinchilla pancreas by
RT chemical assay.";
RL Peptides 11:683-685(1990).
CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
CC THE BLOOD SUGAR LEVEL.
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; A60413; GCCB.
DR HSSP; P01275; 1BH0.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone.
SQ SEQUENCE 29 AA; 3478 MW; 19ECF4DABB752B27 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KHL 15
 |||
Db 12 KHL 14

RESULT 24

IPYR_DESVH

ID IPYR_DESVH STANDARD; PRT; 29 AA.
AC P19371;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-

DE hydrolase) (PPase) (Fragment).
 OS Desulfovibrio vulgaris (strain Hildenborough).
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OX NCBI_TaxID=882;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90365722; PubMed=2168174;
 RA Liu M.-Y., le Gall J.;
 RT "Purification and characterization of two proteins with inorganic
 RT pyrophosphatase activity from Desulfovibrio vulgaris: rubrerythrin
 RT and a new, highly active, enzyme."
 RL Biochem. Biophys. Res. Commun. 171:313-318(1990).
 CC -!- FUNCTION: INORGANIC PYROPHOSPHATASE IS AN ESSENTIAL ENZYME FOR THE
 CC ACTIVATION OF SULFATE BY SULFATE REDUCING BACTERIA. THIS IS A HIGH
 CC ACTIVITY PYROPHOSPHATASE.
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
 DR PIR; A35687; A35687.
 DR HAMAP; MF_00209; -; 1.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR PROSITE; PS00387; PPASE; PARTIAL.
 KW Hydrolase; Periplasmic.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3201 MW; 3FC5792360F2227B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEI 5
 |||
 Db 15 SEI 17

RESULT 25

NUO1_SOLTU
 ID NUO1_SOLTU STANDARD; PRT; 29 AA.
 AC P80267;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 14 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Complex I-14KD) (CI-14KD) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Bintje; TISSUE=Tuber;
 RX MEDLINE=94124587; PubMed=8294484;
 RA Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A.,
 RA Grohmann L.;
 RT "Purification of the NADH:ubiquinone oxidoreductase (complex I) of
 RT the respiratory chain from the inner mitochondrial membrane of

RT Solanum tuberosum.";
 RL J. Biol. Chem. 269:2263-2269(1994).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER
 CC MEMBRANE.
 DR PIR; I49732; I49732.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3269 MW; E2B4DFB558D423D4 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
 |||
 Db 2 RKK 4

RESULT 26

P2SM_LOXIN

ID P2SM LOXIN STANDARD; PRT; 29 AA.
 AC P83046;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sphingomyelinase P2 (EC 3.1.4.12) (Fragment).
 OS Loxosceles intermedia (Spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Haplogynae; Sicariidae; Loxosceles.
 OX NCBI_TaxID=58218;
 RN [1]
 RP SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, COFACTOR, SUBCELLULAR
 RP LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Venom;
 RX MEDLINE=99009277; PubMed=9790962;
 RA Tambourgi D.V., Magnoli F.C., van den Berg C.W., Morgan B.P.,
 RA de Araujo P.S., Alves E.W., Da Silva W.D.;
 RT "Sphingomyelinases in the venom of the spider Loxosceles intermedia
 RT are responsible for both dermonecrosis and complement-dependent
 RT hemolysis.";
 RL Biochem. Biophys. Res. Commun. 251:366-373(1998).
 CC -!- FUNCTION: Has sphingomyelinase activity. Induces complement-
 CC dependent hemolysis and dermonecrosis.
 CC -!- CATALYTIC ACTIVITY: Sphingomyelin + H(2)O = N-acylsphingosine +
 CC choline phosphate.
 CC -!- COFACTOR: Calcium ion.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 KW Hydrolase; Toxin; Calcium; Hemolysis.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3281 MW; 4488EDD619BD2398 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NLG 12
|||
Db 25 NLG 27

RESULT 27

PCG4_PACGO

ID PCG4_PACGO STANDARD; PRT; 29 AA.
AC P82417;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G4.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: HAS ACTIVITY AGAINST SOME GRAM-POSITIVE BACTERIA
CC AND S.CEREVISIAE. HAS A NON-HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3163.87; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 29 AA; 3165 MW; 7037D0B855072AF8 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
|||
Db 11 EWL 13

RESULT 28

SODC_OLEEU

ID SODC_OLEEU STANDARD; PRT; 29 AA.
AC P80740;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Allergen Ole e 5) (Ole e
DE V) (Fragment).

OS Olea europaea (Common olive).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Lamiales; Oleaceae; Olea.
 OX NCBI_TaxID=4146;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pollen;
 RX MEDLINE=98160390; PubMed=9500754;
 RA Boluda L., Alonso C., Fernandez-Caldas E.;
 RT "Purification, characterization, and partial sequencing of two new
 RT allergens of Olea europaea.";
 RL J. Allergy Clin. Immunol. 101:210-216(1998).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems (By similarity).
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
 DR InterPro; IPR001424; SOD_CU_ZN.
 DR Pfam; PF00080; sodcu; 1.
 DR PROSITE; PS00087; SOD_CU_ZN_1; PARTIAL.
 DR PROSITE; PS00332; SOD_CU_ZN_2; PARTIAL.
 KW Antioxidant; Oxidoreductase; Metal-binding; Copper; Zinc; Allergen.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 2973 MW; 836C7A193EDAD71E CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 7 LNS 9

RESULT 29
 TL16_SPIOL
 ID TL16_SPIOL STANDARD; PRT; 29 AA.
 AC P81834;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thylakoid lumenal 16.5 kDa protein (P16.5) (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Leaf;
 RX MEDLINE=98175931; PubMed=9506969;
 RA Kieselbach T., Hagman A., Andersson B., Schroeder W.P.;
 RT "The thylakoid lumen of chloroplasts. Isolation and
 RT characterization.";
 RL J. Biol. Chem. 273:6710-6716(1998).

CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
KW Chloroplast; Thylakoid.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3464 MW; 58B785764E2623E3 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
|||
Db 19 RKK 21

RESULT 30

CBAL_BACST

ID CBAL_BACST STANDARD; PRT; 30 AA.
AC P13722;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-JAN-1990 (Rel. 13, Last annotation update)
DE Alanine carboxypeptidase (EC 3.4.17.6) (Fragment).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE.
RX MEDLINE=81117303; PubMed=6780559;
RA Waxman D.J., Strominger J.L.;
RT "Primary structure of the COOH-terminal membranous segment of a
RT penicillin-sensitive enzyme purified from two Bacilli."
RL J. Biol. Chem. 256:2067-2077(1981).
CC -!- CATALYTIC ACTIVITY: Peptidyl-L-alanine + H(2)O = peptide + L-
CC alanine.
KW Hydrolase; Carboxypeptidase.
FT NON_TER 1 1
SQ SEQUENCE 30 AA; 3367 MW; 6836A3D736CA8326 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SMR 19
|||
Db 7 SMR 9

RESULT 31

DMS3_PHYSA

ID DMS3_PHYSA STANDARD; PRT; 30 AA.
AC P80279;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dermaseptin 3 (DS III).
OS Phyllomedusa sauvagei (Sauvage's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Phyllomedusinae; Phyllomedusa.
 OX NCBI_TaxID=8395;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=94139686; PubMed=8306981;
 RA Mor A., Nicolas P.;
 RT "Isolation and structure of novel defensive peptides from frog skin.";
 RL Eur. J. Biochem. 219:145-154(1994).
 CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
 CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE
 CC FUNCTIONS WITH ITS AMPHIPATIC STRUCTURE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
 CC Dermaseptin subfamily.
 KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.
 SQ SEQUENCE 30 AA; 3024 MW; FD5F190C3DCBB0D7 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKL 28
 |||
 Db 23 KKL 25

RESULT 32

FTN_BACFR

ID FTN_BACFR STANDARD; PRT; 30 AA.
 AC P28733;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ferritin like protein (Fragment).
 OS Bacteroides fragilis.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=817;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=20656-2-1;
 RX MEDLINE=92406001; PubMed=1526453;
 RA Rocha E.R., Andrews S.C., Keen J.N., Brock J.H.;
 RT "Isolation of a ferritin from Bacteroides fragilis."
 RL FEMS Microbiol. Lett. 74:207-212(1992).
 CC -!- FUNCTION: MAY ALLEVIATE IRON TOXICITY IN THE PRESENCE OF
 CC OXYGEN.
 CC -!- COFACTOR: BINDS ABOUT THREE IRON ATOMS PER MOLECULE.
 CC -!- SUBUNIT: FORMS OLIGOMERS OF ABOUT 400 kDa (THE MONOMER IS ABOUT
 CC 17 kDa).
 CC -!- SIMILARITY: BELONGS TO THE FERRITIN FAMILY. PROKARYOTIC SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
 DR InterPro; IPR001519; Ferritin.
 DR Pfam; PF00210; ferritin; 1.

DR PROSITE; PS50905; FERRITIN_LIKE; 1.
 KW Iron storage; Iron; Metal-binding.
 FT DOMAIN 1 >30 FERRITIN-LIKE DIIRON.
 FT METAL 17 17 IRON (BY SIMILARITY).
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3529 MW; C70505B5696EFC4F CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQ 29
 |||
 Db 5 KLQ 7

RESULT 33

GLUM_ANGAN

ID GLUM_ANGAN STANDARD; PRT; 30 AA.
 AC P41521;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glucagon-like peptide (GLP).
 OS Anguilla anguilla (European freshwater eel), and
 OS Anguilla rostrata (American eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC Anguilla.
 OX NCBI_TaxID=7936, 7938;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=A.anguilla, and A.rostrata;
 RC TISSUE=Pancreas;
 RX MEDLINE=91340068; PubMed=1874385;
 RA Conlon J.M., Andrews P.C., Thim L., Moon T.W.;
 RT "The primary structure of glucagon-like peptide but not insulin has
 RT been conserved between the American eel, Anguilla rostrata and the
 RT European eel, Anguilla anguilla."
 RL Gen. Comp. Endocrinol. 82:23-32(1991).
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; B61125; B61125.
 DR PIR; C61125; C61125.
 DR HSSP; P01275; 1BH0.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation.
 FT MOD_RES 30 30 AMIDATION.
 SQ SEQUENCE 30 AA; 3376 MW; 592DA5EABD6E49D0 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQD 30

Db |||
14 LQD 16

RESULT 34

OTCC_AERPU

ID OTCC_AERPU STANDARD; PRT; 30 AA.

AC P11726;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ornithine carbamoyltransferase, catabolic (EC 2.1.3.3) (OTCase)

DE (Fragment).

OS Aeromonas punctata (Aeromonas caviae).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;

OC Aeromonadaceae; Aeromonas.

OX NCBI_TaxID=648;

RN [1]

RP SEQUENCE.

RC STRAIN=NCIB 9232;

RX MEDLINE=85104799; PubMed=3968036;

RA Falmagne P., Portetelle D., Stalon V.;

RT "Immunological and structural relatedness of catabolic ornithine

RT carbamoyltransferases and the anabolic enzymes of enterobacteria.";

RL J. Bacteriol. 161:714-719(1985).

CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate

CC + L-citrulline.

CC -!- PATHWAY: Arginine degradation via arginine deiminase; second step.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.

DR InterPro; IPR006130; Asp/Orn_COTranf.

DR InterPro; IPR006132; OTCace_P.

DR Pfam; PF02729; OTCace_N; 1.

DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; PARTIAL.

KW Transferase; Arginine metabolism.

FT NON_TER 30 30

SQ SEQUENCE 30 AA; 3654 MW; 673CB989FE72F9C1 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 5.4e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EIQ 6

Db |||
19 EIQ 21

RESULT 35

PCG2_PACGO

ID PCG2_PACGO STANDARD; PRT; 30 AA.

AC P82415;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ponericin G2.

OS Pachycondyla goeldii (Ponerine ant).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
 OC Ponerinae; Pachycondyla.
 OX NCBI_TaxID=118888;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Venom;
 RX MEDLINE=21264562; PubMed=11279030;
 RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
 RA Longeon A., Chafotte A., Dejean A., Rossier J.;
 RT "Ponericins, new antibacterial and insecticidal peptides from the
 RT venom of the ant *Pachycondyla goeldii*.";
 RL J. Biol. Chem. 276:17823-17829(2001).
 CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
 CC AND GRAM-NEGATIVE BACTERIA AND *S.CEREVISIAE*. HAS INSECTICIDAL
 CC AND NON-HEMOLYTIC ACTIVITIES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=3306.56; METHOD=MALDI.
 KW Antibiotic; Insect immunity; Fungicide.
 SQ SEQUENCE 30 AA; 3308 MW; A12CD4D0BAF40B5D CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
 |||
 Db 11 EWL 13

RESULT 36

PCG3_PACGO

ID PCG3_PACGO STANDARD; PRT; 30 AA.
 AC P82416;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ponericin G3.
 OS *Pachycondyla goeldii* (Ponerine ant).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
 OC Ponerinae; Pachycondyla.
 OX NCBI_TaxID=118888;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Venom;
 RX MEDLINE=21264562; PubMed=11279030;
 RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
 RA Longeon A., Chafotte A., Dejean A., Rossier J.;
 RT "Ponericins, new antibacterial and insecticidal peptides from the
 RT venom of the ant *Pachycondyla goeldii*.";
 RL J. Biol. Chem. 276:17823-17829(2001).
 CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
 CC AND GRAM-NEGATIVE BACTERIA AND *S.CEREVISIAE*. HAS INSECTICIDAL
 CC AND NON-HEMOLYTIC ACTIVITIES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=3381.36; METHOD=MALDI.
 KW Antibiotic; Insect immunity; Fungicide.

SQ SEQUENCE 30 AA; 3383 MW; BC0463D0AF140B53 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24

|||

Db 11 EWL 13

RESULT 37

PRT1_CLUPA

ID PRT1_CLUPA STANDARD; PRT; 30 AA.

AC P02335;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Protamine YII (Clupeine YII).

OS Clupea pallasii (Pacific herring), and

OS Clupea harengus (Atlantic herring).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;

OC Clupea.

OX NCBI_TaxID=30724, 7950;

RN [1]

RP SEQUENCE.

RC SPECIES=C.pallasii;

RX MEDLINE=73223106; PubMed=4664740;

RA Suzuki K., Ando T.;

RT "Studies on protamines. XVI. The complete amino acid sequence of

RT clupeine YII.";

RL J. Biochem. 72:1419-1432(1972).

RN [2]

RP SEQUENCE.

RC SPECIES=C.harengus;

RA Chang W.J., Nukushina M., Ishii S., Nakahara C., Ando T.;

RL Submitted (AUG-1970) to the PIR data bank.

CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF

CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- TISSUE SPECIFICITY: Testis.

DR PIR; A37575; CLHR2A.

DR PIR; A38052; CLHRY2.

KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;

KW Testis; DNA condensation; Nuclear protein.

SQ SEQUENCE 30 AA; 4049 MW; 7F9BBB80F3ADA566 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 RRV 21

|||

Db 18 RRV 20

RESULT 38

PRTB_ONCMY

ID PRTB_ONCMY STANDARD; PRT; 30 AA.

AC P12819;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Protamine 1A (Protamine PRTP43/PPC 2E).

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE.

RX MEDLINE=86274711; PubMed=3755398;

RA McKay D.J., Renaux B.S., Dixon G.H.;

RT "Rainbow trout protamines. Amino acid sequences of six distinct

RT proteins from a single testis.";

RL Eur. J. Biochem. 158:361-366(1986).

RN [2]

RP SEQUENCE FROM N.A. (CLONE PRTP43).

RX MEDLINE=81198983; PubMed=6262730;

RA Gedamu L., Wosnick M.A., Connor W., Watson D.C., Dixon G.H.,

RA Iatrou K.;

RT "Molecular analysis of the protamine multi-gene family in rainbow

RT trout testis.";

RL Nucleic Acids Res. 9:1463-1482(1981).

RN [3]

RP SEQUENCE FROM N.A. (CLONE PPC 2E).

RX MEDLINE=82030654; PubMed=7287661;

RA Sakai M., Fujii-Kuriyama Y., Saito T., Muramatsu M.;

RT "Closely related mRNA sequences of protamines in rainbow trout

RT testis.";

RL J. Biochem. 89:1863-1868(1981).

CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF

CC SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT

CC SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.

CC -!- SUBCELLULAR LOCATION: Nuclear.

CC -!- TISSUE SPECIFICITY: Testis.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; K03052; AAA49607.1; -.

DR EMBL; K03051; AAA49606.1; -.

DR PIR; B02673; ITRC2.

DR PIR; I51349; I51349.

KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;

KW Testis; DNA condensation; Nuclear protein.

FT INIT_MET 0 0

SQ SEQUENCE 30 AA; 4050 MW; 0EBCBF9DC78B5947 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 RRV 21
|||
Db 8 RRV 10

RESULT 39

PSAM_PORPU

ID PSAM_PORPU STANDARD; PRT; 30 AA.

AC P51395;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Photosystem I reaction centre subunit XII (PSI-M).

GN PSAM.

OS Porphyra purpurea.

OG Chloroplast.

OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.

OX NCBI_TaxID=2787;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Avonport;

RA Reith M.E., Munholland J.;

RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast
genome.";

RL Plant Mol. Biol. Rep. 13:333-335(1995).

CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC

DR EMBL; U38804; AAC08281.1; -.

DR PIR; S73316; S73316.

KW Photosystem I; Photosynthesis; Chloroplast.

SQ SEQUENCE 30 AA; 3338 MW; 8D1930479D8A5527 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGK 13
|||
Db 24 LGK 26

RESULT 40

RL18_HALCU

ID RL18_HALCU STANDARD; PRT; 30 AA.
 AC P05970;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 50S ribosomal protein L18P (HCUL18) (HL13) (Fragment).
 GN RPL18P.
 OS Halobacterium cutirubrum.
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=2242;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79045279; PubMed=152199;
 RA Smith N., Matheson A.T., Yaguchi M., Willick G., Nazar R.N.;
 RT "The 5-S RNA-protein complex from an extreme halophile,
 RT Halobacterium cutirubrum. Purification and characterization."
 RL Eur. J. Biochem. 89:501-509(1978).
 CC -!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
 DR PIR; S07217; S07217.
 KW Ribosomal protein.
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3624 MW; 3A50079B1569CB74 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MRR 20
 |||
 Db 10 MRR 12

Search completed: January 14, 2004, 10:35:34
 Job time : 6.61371 secs